

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2004, 15:12:04 ; Search time 8805 Seconds  
(without alignments)  
11326.783 Million cell updates/sec

Title: US-10-043-715-1\_COPY\_157700\_160000  
Perfect score: 2301  
Sequence: 1 ctgaatgatgtctcccaagt.....tagctccacggagagccct 2301

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.scs.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sv.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2301	100.0	186510	9	HS451B15	Z98050 Human DNA s
2	2292.6	99.6	109047	2	HSJ19F5	AL078592 Homo sapi
3	2273.2	98.8	10006	9	AY434104	AY434104 Homo sapi
4	2241.6	97.4	12461	9	HUMEDN1B	J05008 Homo sapien
5	2230	96.9	12460	6	A98526	A98526 Sequence 1
6	2230	96.9	12460	6	BD080748	BD080748 Antisense
7	662.4	28.8	684	9	HUMETN3	M25379 Human endot
8	411.4	17.9	1425	9	AC036851	BC036851 Homo sapi
9	263.2	11.4	259474	2	AC095692	AC095692 Rattus no
10	241	10.5	1330	9	HUMETN4	M25380 Human endot
11	239	10.4	237384	2	AC131424	AC131424 Rattus no
12	166	7.2	266	4	AF130760	AF130760 Equus cab
13	157.4	6.8	636	6	BD094780	BD094780 The cell
14	157.4	6.8	636	6	BD096322	BD096322 Cells cap
15	157.4	6.8	1167	9	HSET	Y00749 Human mRNA
16	157.4	6.8	1175	6	E02620	E02620 DNA encodin
17	157.4	6.8	1251	6	AX587988	AX587988 Sequence
18	157.4	6.8	1251	9	S56805	S56805 preproendot
19	157.4	6.8	1334	9	BC009720	BC009720 Homo sapi
20	150.2	6.5	230	9	MFU20579	U20579 Macaca fasc
21	125	5.4	139	10	D7083952	D70840 Mus musculu
22	123.6	5.4	98530	2	AC113088	AC113088 Mus muscu
23	112.4	4.9	1936	4	AB115087	AB115087 Canis fam
24	111.2	4.8	447	10	S82654	S82654 preproendot
25	107.2	4.7	949	4	BTENDOTH	X52942 Bovine mRNA
26	107.2	4.7	1762	4	BTENDO	X52740 Bovine mRNA
27	107.2	4.7	2023	4	S37093	S37093 preproendot
28	103	4.5	1385	10	RATET1	M64711 Rat endothe
29	101.4	4.4	695	6	AX525996	AX525996 Sequence
30	100.8	4.4	749	6	E02619	E02619 DNA encodin
31	100.8	4.4	1838	4	SSET	X07383 Porcine mRN
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33	99.2	4.3	1770	10	MMU35233	U35233 Mus musculu
34	99.2	4.3	2153	10	BC029547	BC029547 Mus muscu
35	99	4.3	225	11	AB031407	AB031407 Sus scrof
36	97.6	4.2	1143	4	AF329468	AF329468 Ovis arie
37	96.8	4.2	1639	4	OCET1	X59931 O.cuniculus
38	96	4.2	1586	10	D43775	D43775 Mouse mRNA
39	93.4	4.1	319	10	AF122903	AF122903 Rattus no
40	88.2	3.8	288	4	AF333433	AF333433 Canis fam
41	79	3.4	1231	10	D7083954	D70842 Mus musculu
42	73	3.2	236	4	AF320770	AF320770 Felis cat
43	70	3.0	154	10	D7083953	D70841 Mus musculu
44	66.6	2.9	7218	6	I66494	I66494 Sequence 14
45	58	2.5	1141	6	AX083744	AX083744 Sequence

ALIGNMENTS

RESULT 1	HS451B15	HS451B15	186510 bp	DNA	linear	PRI 05-JUN-2003
LOCUS						
DEFINITION						Human DNA sequence from clone RP3-451B15 on chromosome 6p24
						Contains the 3' end of the HIVEP1 gene for human immunodeficiency
						virus type 1 enhancer-binding protein 1, the EDN1 gene for
						endothelin 1 (ET1) and a SMR3 suppressor of mlf two 3 homolog 1
						(yeast) (SMT3H1) pseudogene, complete sequence.
ACCESSION	Z98050					
VERSION	Z98050.1	GI:2791272				
KEYWORDS	HTG; EDN1; endothelin;	ET1; HIVEP1; SMT3H1.				
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					

# REFERENCE AUTHORS TITLE JOURNAL

1 (bases 1 to 186510)  
Tubby,B.  
Direct Submission  
Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Jan 18, 1998 this sequence version replaced gi:2558561.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
-----

## COMMENT

During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the rare  
assembly was confirmed by restriction digest, except on the rare  
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information  
on the WormPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence

was generated from part of bacterial clone contigs of human  
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping  
Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>

RP3-451B15 is from the library RPCI-3 constructed by the group of  
Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-451B15.

## FEATURES source

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[illegible]

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Qy	1441	GAACACTCTCTGAGTATTTTACTACTGATTTGTGGGCAGCCTCAGCTATCGGTTCTTTC	1500
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Qy	1861	GAGAACACGACAACTCTAGTTATTTAAACCTGTATTATCTGCCCACTTCCCTTA	1920
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Qy	1921	GACTTGACCATATGACCCCTCGCTCCCATCTAAGCATAGGGCAGGCTTATTTTACA	1980
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Qy	2101	GTGATTTTTTTAAATAACATTTGTTTTCTCTATCTCTGTTTATTAGTTCGAGACCAT	2160
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Qy	2161	GAGAAACAGCGTCAAAATCATTTTTCATGATCCCAAGCTGAAAGGCAAGCCCTCCAGA	2220
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Qy	2281	ATAGCCTCCACGAGAGCC	2299
Db	135	ATAGCCTCCACGAGAGCC	117

LOCUS AY434104 10006 bp DNA linear PRI 20-OCT-2003  
DEFINITION Homo sapiens endothelin 1 (EDN1) gene, complete cds.  
ACCESSION AY434104  
VERSION AY434104.1 GI:37654537  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10006)  
Rieder, M.J., Livingston, R.J., Daniels, M.R., Chung, M.-W.,  
Miyamoto, K.E., Nguyen, C.P., Nguyen, D.A., Foel, C.L., Robertson, P.D.,  
Schackwitz, W.S., Sherwood, J.K., Wittrak, L.A. and Nickerson, D.A.  
Direct Submission  
TITLE Submitted (09-OCT-2003) Genome Sciences, University of Washington,  
JOURNAL 1705 NE Pacific, Seattle, WA 98195, USA.  
COMMENT To cite this work please use: NIEHS-SNPs, Environmental Genome  
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA  
(URL: <http://esg.gs.washington.edu>).  
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Qy	419	GAATGTTTTCTCTGTGTATTTTAAACAGGCCTGAAGACATTTAGGAGAAAGACTGGAAT	478
Db	5755	GAATGTTTTCTCTGTGTATTTTAAACAGGCCTGAAGACATTTAGGAGAAAGACTGGAAT	5814
Qy	479	AATCATPAAGAAAGGAAAGACTGTTCCAAGCTTGGGAAAAAGTGTATTTATCAGCAGTTA	538
Db	5815	AATCATPAAGAAAGGAAAGACTGTTCCAAGCTTGGGAAAAAGTGTATTTATCAGCAGTTA	5874
Qy	539	GTGAGAGGAAGAAAAATCAGAAAGTTCAAGAGAAACCTTAAGACAAACCAGGTAAAGAG	598
Db	5875	GTGAGAGGAAGAAAAATCAGAAAGTTCAAGAGAAACCTTAAGACAAACCAGGTAAAGAG	5934
Qy	599	GGAAAGGAAAAAATTAGTTPAAGAGTTTCAAGAAACAACTAGCCCCAGTCAGTGATGCC	658
Db	5935	GGAAAGGAAAAAATTAGTTPAAGAGTTTCAAGAAACAACTAGCCCCAGTCAGTGATGCC	5994
Qy	659	AGCAGCCTGTCTCCAGCCCTTTTACCGCGGCAGGTGAAGACATTTAGAAAACAGTAGC	718
Db	5995	AGCAGCCTGTCTCCAGCCCTTTTACCGCGGCAGGTGAAGACATTTAGAAAACAGTAGC	6054
Qy	719	AGAGGAGATCTATGCAATCCTATAGATTAAGAGGAGCAAAAGAAATCCCTCTTAAATATTTC	778
Db	6055	AGAGGAGATCTATGCAATCCTATAGATTAAGAGGAGCAAAAGAAATCCCTCTTAAATATTTC	6114
Qy	779	CATGAAGCTCTGAAATGCAAAACGATGTCCTCTGTACTTTTAGCACATACCAATTCATCT	838
Db	6115	CATGAAGCTCTGAAATGCAAAACGATGTCCTCTGTACTTTTAGCACATACCAATTCATCT	6174
Qy	839	ACAGGTAGATTTCCCAACCAAAATATATCAGAGATGCCCTTTGTCTATGGGTTATATACA	898
Db	6175	ACAGGTAGATTTCCCAACCAAAATATATCAGAGATGCCCTTTGTCTATGGGTTATATACA	6234
Qy	899	GCCCTTTGCCCTCTGTAGTCAATGTATTACCACTTCCCTGAGAAATCGAAAATCATTTT	958
Db	6235	GCCCTTTGCCCTCTGTAGTCAATGTATTACCACTTCCCTGAGAAATCGAAAATCATTTT	6294
Qy	959	GGGGAGCGGACATTTAGAAAAAGAAATCAAAGTGTATGGATTAATCAAATTTCTTCAATAG	1018
Db	6295	GGGGAGCGGACATTTAGAAAAAGAAATCAAAGTGTATGGATTAATCAAATTTCTTCAATAG	6354
Qy	1019	TTGCAGTTATTAGATGGCCAAAGGAAAAATAAGTCATTAGTAGGGTTGGTAGAATTT	1078
Db	6355	TTGCAGTTATTAGATGGCCAAAGGAAAAATAAGTCATTAGTAGGGTTGGTAGAATTT	6414
Qy	1079	AGAACATGCTGTTTTTCAGGTTTATGGCTTTTTTTTTTTTTTTTTTTTTTAAATAGGAAA	1138
Db	6415	AGAACATGCTGTTTTTCAGGTTTATGGCTTTTTTTTTTTTTTTTTTTTTTAAATAGGAAA	6474
Qy	1139	TGTGTTTTGTGAGAGCCAAATGTCATTCCAAAAGCTCTCTTTTTTCTGTGTCAGTCATG	1198
Db	6475	TGTGTTTTGTGAGAGCCAAATGTCATTCCAAAAGCTCTCTTTTTTCTGTGTCAGTCATG	6534
Qy	1199	TGCTGGGACAGAGAGGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGGCTGCTCT	1258
Db	6535	TGCTGGGACAGAGAGGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGGCTGCTCT	6594
Qy	1259	TTGGTGATTAACCTTCCAAATCCTAAACCTTTTTTGGAAITCAACAGCTCAAGAGGAAAC	1318
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QY	1439	ATGAACTACTTCTGAGTTATTTACTACTGATTTCTGCGGAGCTCAGCTATCGGTTCT	1498
DB	6775	ATGAACTACTTCTGAGTTATTTACTACTGATTTCTGCGGAGCTCAGCTATCGGTTCT	6834
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DB	6835	TCACACCTGCTTATGAGAGTATCCATATTTATGTCGAGGCCAGTAACTCCTCCACGA	6894
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DB	7015	AAATCTTTTAAATAATATGCAATAAGTATTTGCTCTGGGCTACTGTATGCTTTT	7074
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QY	1859	CGGAAGAACCCAGACCACTCTAGTTATTTTAAACCTGTATTTACTGCCACCTCCCT	1918
DB	7195	CGGAAGAACCCAGACCACTCTAGTTATTTTAAACCTGTATTTACTGCCACCTCCCT	7254
QY	1919	TAGACTTGACCATATGACCCCTCGCTCCCATTTCTAAGCATAGGGCAGGCTTTT	1978
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QY	2039	ACAACCCAGATTGAGGTTTGTGTGCGCAGATTTCTAATTTTACATGTTTCTTTGCCAA	2098
DB	7375	ACAACCCAGATTGAGGTTTGTGTGCGCAGATTTCTAATTTTACATGTTTCTTTGCCAA	7434
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DB	7435	GGGTGA-TTTTTTAAATAAATGTTTCTTCTATCTTCTTCTTCTTCTTCTTCTTCT	7494
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DB	7495	CATGAGAACCCGTCATATCTTTTCTGATCCCAAGCTGAAAGGCAAGCCCTCCAG	7554
QY	2218	AGAGCGTTATGACCCCAACCCAGACCATTTGGTGAAGACCTTTGGGGGCTGTCTGAA	2277
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		Db	7356	TGCTTTTCAATCAGTTTAAACAGCTCTCTGAACCTCTCTATCATGTTACTGCTTCTCTG	7415
protein_bind		Qy	361	TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAAGGTAAAGCTGAATATAACATTCCTGA	420
		Db	7416	TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAAGGTAAAGCTGAATATAACATTCCTGA	7475
exon		Qy	421	AATGTTTTTCTTGTGTATTTTAAACAGGCTGAAGACATTTATGAGAAAGACTTGAATAA	480
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exon		Qy	841	AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCTTTTGTTCATTGGGTATATACAGC	900
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protein_bind		Qy	901	CTTTGCTCTCTGAGTCAATGTATTTTACACTTTTCCCTGAGAAATCGAAAAATCATTTTG	960
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		Qy	1256	TCCTTGGTATACCTTCCAAATCTTAACTTTTTTGGAAATTCACAAAGCTCAAGAGAGA	1315
		Db	8316	TCCTTGGTATACCTTCCAAATCTTAACTTTTTTGGAAATTCACAAAGCTCAAGAGAGA	8375
		Qy	1316	AACCTACTCTCTGATCTACAGATGTTCTGCAATTTTCTATCATGCTCTATGAAACTTC	1375
		Db	8376	AACCTACTCTCTGATCTACAGATGTTCTGCAATTTTCTATCATGCTCTATGAAACTTC	8435

## ORIGIN

Query Match	97.4%;	Score	2241.6;	DB	9;	Length	12461;
Best Local Similarity	99.3%;	Pred.	No. 0;				
Matches	2294;	Conservative	1;	Mismatches	5;	Indels	10;
						Gaps	4;
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Db	7056	CTGAAATGATGCTCCCAAGTGTATGTGATGAGCTCCTTGTGTCGCCAGTGGAAATAGGTG	7115				
Qy	61	TGTCATGTCATTTTAAAGACTATTAATACACTAATATAGTTTCTCTCTCTTGG	120				
Db	7116	TGTCATGTCATTTTAAAGACTATTAATACACTAATATAGTTTCTCTCTCTTGG	7175				
Qy	121	ATAATAGGACGTTGTTCCGATGACCTTGAAGCCCTTAGTCCCAAGAGACCTTGGAGA	180				
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 12460)  
AUTHORS Higenbottam, T. and McCormack, K.  
TITLE ANTISENSE TREATMENT OF PULMONARY HYPERTENSION  
JOURNAL Patent: WO 9911778-A 1 11-MAR-1999;  
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QY 2272 TCTGAGCCATAGCTCCACGAGAGCCCT 2301  
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RESULT 6  
BD080748 12460 bp DNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION Antisense remedy of pulmonary hypertension.  
ACCESSION BD080748  
VERSION BD080748.1 GI:22626351  
KEYWORDS JP 2001515011-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 12460)  
AUTHORS Higendotam,T., McCormack,K. and Smith,A.  
TITLE Antisense remedy of pulmonary hypertension  
JOURNAL Patent: JP 2001515011-A 1 18-SEP-2001;  
UNIVERSITY OF SHEFFIELD  
COMMENT OS Homo sapiens (human)  
PN JP 2001515011-A/1  
PD 18-SEP-2001  
PF 02-SEP-1998 JP 2000508789  
PR 02-SEP-1997 GB 9718487.3  
PI TIMOTHY HIGENBOTTAM, KEITH MCCORMACK, ADRIAN SMITH PC  
A61K31/708,A61M11/00,A61M15/00,A61P3/06,C12N15/09,C12N15/00 CC  
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CC Topology: Linear;  
CC Antisense remedy of pulmonary hypertension  
FH Key Location/Qualifiers  
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FT /organism='Homo sapiens (human)'.  
FEATURES  
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/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'

Query Match 96.9%; Score 2230; DB 6; Length 12460;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2294; Conservative 0; Mismatches 5; Indels 11; Gaps 5;  
QY 1 CTGAAATGATGCTCCCAAGTGTATGATGAGCTCTTGTGTGCCACTGGAATAGGTC 60

Db 7056 CTGAATGATGCTCCCAAGTCTATGTGATGAGCTCCTTGTGTGCCAGTGGAAATAGGTG 7115  
QY 61 TGTCCATGTGTCATTTTAAAGACTATTAAATACATAATATAGTTTCTTCTCTTTGG 120  
Db 7116 TGTCCATGTGTCATTTTAAAGACTATTAAATACATAATATAGTTTCTTCTCTTTGG 7175  
QY 121 ATATAGGACGCTGTTCCTGATGAGCTTGGAGCCCTAGTCCAAAGAGAGCCCTTGGAGA 180  
Db 7176 ATATAGGACGCTGTTCCTGATGAGCTTGGAGCCCTAGTCCAAAGAGAGCCCTTGGAGA 7235  
QY 181 ATTTACTTTCCCAAGGCAACAGACCGTGAAATAGATGCCAATGTGTCAGCCAAAAG 240  
Db 7236 ATTTACTTTCCCAAGGCAACAGACCGTGAGATAGATGCCAATGTGTCAGCCAAAAG 7295  
QY 241 ACAAGAAGTGTGNAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACCTT 300  
Db 7296 ACAAGAAGTGTGNAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACCTT 7355  
QY 301 TGCCTTTCAATCAGTTTAAAGCCTTCTGAACCTCTTCTATCATGTGCTGCTTCTG 360  
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QY 361 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGTAAGCTGAATATTAACATTTGCTGA 420  
Db 7416 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGTAAGCTGAATATTAACATTTGCTGA 7475  
QY 421 AATGTTTTTCTGTGTATTTTAAAGGCTGAAAGATTAAGTGAAGAAAGCTGGAATAA 480  
Db 7476 AATGTTTTTCTGTGTATTTTAAAGGCTGAAAGATTAAGTGAAGAAAGCTGGAATAA 7535  
QY 481 TCATAAGAAAGAAAGACTGTTCAGACTTTGGAAAGTGTATTTATCAGCAGTTAGT 540  
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Db 7596 GAGAGAGAAAGAAATCAGAGAGTTTCAAGAGACACTTAAGACAAACCCAGGTAAAGGG 7655  
QY 601 AAGGAGAGAAAGAAATAGGTAAAGGTTTCAAGAGACACTTAAGACAAACCCAGGTAAAGGG 660  
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QY 721 AGGAGATCTATGATCTTATAGATTAAAGAGGAGAAAGAAATCCCTCTTAAATATTTCCA 780  
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QY 1021 GCAGTTATTCAGATGGCCAAAGGAAATAAAGTCAATAGATAGGTTGTAGAAATTTAG 1080  
Db 8076 GCAGTTATTCAGATGGCCAAAGGAAATAAAGTCAATAGATAGGTTGTAGAAATTTAG 8135  
QY 1081 AACATGCTGTTTTTTCAGGTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGG 1135  
Db 8136 AACATGCTGTTTTTTCAGGTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGG 8195

QY 1136 AAATGCTGTTTGTGAGAGCCAAATGTCATTTCCAAAAGCTCTCTCTTTTCTGCTCAGTC 1195  
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QY 1496 TCTTCCACACTCTTATGAGAGTATCCATATTTATGTTGCGAGGCCAGTAATGCTCCCA 1555  
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Db 9034 TTTACATGCTTAATAAGATATCACTGAGTTTATCAAGAGTTCGCGGGTGGTG 9093  
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y	2212	CTCCAGAGCGGTTATGTGACCCACACCGAGACATTGGTGACAGACCTTCGGGGCCTG	2271
b	9274	CTCCAGAGCGGTTATGTGACCCACACCGAGACATTGGTGACAGACCTTCGGGGCCTG	9333
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b	9334	TCTGAGGCCATAGCCTCCACGAGAGCCCT	9363
RESULT 7			
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LOCUS	HUMETN3 664 bp DNA linear PRI 08-NOV-1994		
DEFINITION	Human endothelin (ETN) gene, complete cds.		
ACCESSION	M25379 J04819		
VERSION	M25379.1 GI:182256		
KEYWORDS	endothelin.		
SEGMENT	3 of 4		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE	89278161		
PUBMED	2859594		
COMMENT	Original source text: Human leukocyte DNA and human umbilical vein endothelial cell cDNA to mRNA. Draft entry and computer readable copy of sequence [1] kindly submitted by K.D.Bloch (06-AUG-89).		
FEATURES			
source			
prim_transcript			
intron			
exon			
intron			
exon			
intron			
ORIGIN			
Query Match			
Best Local Similarity			
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y	28	GATGAGCTCTTGTCGCCAGTGGAAATAGGTGTGTCCATGTGTCCATTTAAAGACTATT	87
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b	61	AATTACACTAATATAGTTCTTCTCTTGGATTAATAGGACGTTGTCGTATGGAC	120
y	148	TTGGAAGCCCTAGGTCACAGAGAGCCCTGGAGAAATTTACTTCCCAAAAGGCAACAGACC	207

JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1425)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc.mgc@hgrl.nih.gov">nisc.mgc@hgrl.nih.gov</a> Ahter,N., Ayle,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Goufard,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
FEATURES	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a></p> <p>Series: iRAK Plate: 78 Row: M Column: 2.</p> <p>Location/Qualifiers</p> <p>1..1425</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:5405159"</p> <p>/tissue_type="Liver, adenocarcinoma"</p> <p>/clone_lib="NIH MGC_90"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pCMV-SPORT6"</p>
ORIGIN	<p>Query Match 17.9%; Score 411.4; DB 9; Length 1425;</p> <p>Best Local Similarity 99.5%; Pred. No. 8.5e-83;</p> <p>Matches 423; Conservative 0; Mismatches 1; Indels 1; Gaps 1;</p>
QY	1878 TCTAGTTTATTAACCTGATTACTGCTCCCACTCCCTTACATGTCACCATATGACC 1937
Db	1313 TTTAGTTTATTAACCTGATTACTGCTCCCACTCCCTTACATGTCACCATATGACC 1254
QY	1938 CTTGCTCCCATTTAAGCATAGGGGCGGCTTTATTTTACATGTTATAGATATCAC 1997
Db	1253 CTTGCTCCCATTTAAGCATAGGGGCGGCTTTATTTTACATGTTATAGATATCAC 1194
QY	1998 TTGAGGTTTATCAAGAGTTGCGCGGGTGGTGAAGAGTTTCACAA-CCAGATTTCAGGTTT 2056
Db	1193 TTGAGGTTTATCAAGAGTTGCGCGGGTGGTGAAGAGTTTCACAA-CCAGATTTCAGGTTT 1134
QY	2057 TGTGTGCGCAGATCTAAATTTTACATGTTCTTTTCCGAAAGGTTGATTTTTTAAAT 2116
Db	1133 TGTGTGCGCAGATCTAAATTTTACATGTTCTTTTCCGAAAGGTTGATTTTTTAAAT 1074
QY	2117 AACATTGTTTCTTATCTTGTCTTTATAGGTCGGAGACCATGAGAAACGCGTCAAA 2176
Db	1073 AACATTGTTTCTTATCTTGTCTTTATAGGTCGGAGACCATGAGAAACGCGTCAAA 1014
QY	2177 TCATCTTTTTCATGATCCCAAGCTGAAGGCAAGCCCTCCAGAGAGCGTTATGTGACCCAC 2236
Db	1013 TCATCTTTTTCATGATCCCAAGCTGAAGGCAAGCCCTCCAGAGAGCGTTATGTGACCCAC 954
QY	2237 AACCGAGCATTGGTGACAGACCTTCGGGGCTGTCTGAAGCCATAGCTCCACGAGA 2296
Db	953 AACCGAGCATTGGTGACAGACCTTCGGGGCTGTCTGAAGCCATAGCTCCACGAGA 894
QY	2297 GCCCT 2301
Db	893 GCCCT 889
RESULT 9	
AC095692/c	259474 bp DNA linear HTG 13-NOV-2002
LOCUS	Rattus norvegicus clone CH230-9D3, WORKING DRAFT SEQUENCE, 4
DEFINITION	unordered pieces.
ACCESSION	AC095692
VERSION	AC095692.5 GI:24940989
KEYWORDS	HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 259474)
REFERENCE	Muzay,D.Marie., Metker,M.Lee., Abranzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,H., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensheva,L., Louisedge,H., Lozano,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwankweli,O., Okwuonu,G., Olarnpusagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfamkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Sivartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczky,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE	Direct Submission

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 259474)  
Worley, K.C.  
Direct Submission  
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

3 (bases 1 to 259474)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:22727932.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GPAS  
Center clone name: CH230-9D3  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 226564 bases at least Q40  
Consensus quality: 228265 bases at least Q30  
Consensus quality: 229686 bases at least Q20  
Estimated insert size: 232505; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 226873: contig of 226873 bp in length  
\* 226874 226973: gap of unknown length  
\* 226974 240221: contig of 13248 bp in length  
\* 240222 240321: gap of unknown length  
\* 240322 245800: contig of 5479 bp in length  
\* 245801 245900: gap of unknown length  
\* 245901 259474: contig of 13574 bp in length.

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DEFINITION M25380 J04819  
ACCESSION M25380.1 GI:182257  
VERSION 4 of 4  
KEYWORDS endothelin.  
SOURCE Homo sapiens (human)  
SEGMENT 4 of 4  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1330)  
AUTHORS Bloch,K.D., Friedrich,S.P., Lee,M.E., Eddy,R.L., Shows,T.B. and Quettermou,S.T.  
TITLE Structural organization and chromosomal assignment of the gene encoding endothelin  
JOURNAL J. Biol. Chem. 264 (18), 10851-10857 (1989)  
MEDLINE 89278161  
PubMed 2659594  
COMMENT Original source text: Human leukocyte DNA and human umbilical vein endothelial cell cDNA to mRNA.  
Draft entry and computer readable copy of sequence [1] kindly submitted by K.D.Bloch (06-AUG-89).  
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QY 2289 CACGGAGAGCCCT 2301
Db 240 CACGGAGAGCCCT 252

RESULT 11
AC131424
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AC131424
AC131424.4 GI:25138078
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 237384)
Muzny, D., Marie, Metzker, M., Lee, A., Brannon, S., Adams, C., Alder, J.,
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Mawney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
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Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
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Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
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Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G., and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 237384)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (22-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237384)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23194834.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUVH
Center clone name: CH230-248L7
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202780 bases at least Q40
Consensus quality: 204531 bases at least Q30
Consensus quality: 205595 bases at least Q20
Estimated insert size: 206846; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 190059: contig of 190059 bp in length
* 190060 190159: gap of unknown length
* 190160 191371: contig of 1212 bp in length
* 191372 191471: gap of unknown length
* 191472 192435: contig of 2774 bp in length
* 192436 194345: gap of unknown length
* 194346 206754: contig of 12409 bp in length
* 206755 206854: gap of unknown length
* 206855 237384: contig of 30530 bp in length.
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* Location/Qualifiers
* 1 .237384
* /organism="Rattus norvegicus"
FEATURES
source

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ORIGIN
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Matches 1228; Conservative 0; Mismatches 815; Indels 260; Gaps 24;
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Db 42090 TCCGTACTTGTGATATGAGTGTGCCAATGAATGCTCTCTGAATGTAGGCCCAAGGA 42149
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Db 42150 ATTTGAAAGATTAATAGTAGGTAAATATCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 42209
QY 133 TTGTTCCGATGACCTTCGAGCC---CTAGGTCACAGAGAGCCTTTGAGAAATTTACTTTC 189
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QY 190 CCACAAAGCAACAGCCGCTGAAATATAGATGCCAATGTGCTAGCCAAAAGACAAAGAGT 249
Db 42270 CCACAAAGCAACAGCCGCTGAAATATAGATGCCAATGTGCTAGCCAAAAGACAAAGAGT 42329
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QY 730 ATGCATCTCTATAGATTAAGAGGAGAAAGAAATCCCTCTTAAATATTTCCATGAAGCTCT 789
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QY 790 GGAATGCAACCGATGCTCTGTACTTTTAGCACATACCATTTTCATCTACAGGTAGATT 849
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QY 910 TCTGAGTCAATGTATTTACCACTTTCCCTGAGAAATCGAAATATTTTGGGAGCGGAC 969
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Db 43616 TAGGTCTCCCTTAGGCTCCCTAAATTTCTCTCCATCCACCTTTAGCTTCCATT----- 43670
QY 1808 CTGAGTTCTCAGGCGAGGTCACATAGTATGAAGTTGGATGGGCTAGCGGCTACGGAGAAA 1867
Db 43671 -----TCTTCTGTGTTTGAAGAGTCCAGAGGTTAGATGACGCTACTTTAAGCAG 43721
QY 1868 CCAGAACAACTCTAGTTTATTTTAAACCTGTATTTTACTGCCCACTTCCCTTAGACTTGA 1927
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Db 43722 AACATTGGAACTTAACCTCCCTGTAGACATACCTCAGAGCTTCCTCTCCACAGACCAAA 43781
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Db 43782 CAGCATAGACAGCAGCGGTCTATTACACAATAGTCGTAGCCGCTCTTTGAGGATTTATCA 43841
Qy 1988 TAGATATCACTTTGAGGTTTATCAAAAGAGTTCGCGGGGTGTGAAAGTTTACACACAGA 2047
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Qy 2155 GACCATGAGAAACAGCGTCAAAATCATCTTTTCATGATCCCAAGCTGAAAGCGACGCCCTC 2214
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Qy 2215 CAGAGAGCTTATGTAGCCCAACAGCAGACATTTGTCAGACACCTTCGGGCGCTGTCT 2274
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Qy 2275 GAAGCATAGCTTCAACGGAGAG 2297
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RESULT 12
AF130760 266 bp DNA linear MAM 03-FEB-2000
LOCUS
DEFINITION
EQUUS caballus chromosome 20 EDN1 gene, partial sequence.
ACCESSION
AF130760
VERSION
AF130760.1 GI:6855655
KEYWORDS
EQUUS caballus (horse)
ORGANISM
EQUUS caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
1 (bases 1 to 266)
AUTHORS
Caetano, A.R., Shue, Y.L., Lyons, L.A., O'Brien, S.J., Laughlin, T.F.,
Bowling, A.T., and Murray, J.D.
TITLE
A comparative gene map of the horse (EQUUS caballus)
JOURNAL
Genome Res. 9 (12), 1239-1249 (1999)
MEDLINE
20082971
PUBMED
10613847
REFERENCE
2 (bases 1 to 266)
AUTHORS
Caetano, A.R.
DIRECT SUBMISSION
Submitted (25-FEB-1999) Veterinary Genetics Lab., University of
California, Davis, One Shields Ave., Davis, CA 95616, USA
FEATURES
Location/Qualifiers
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Db 61 AACAC--TTTACTTTCAATCAGTTTACAGCTCTCTGGTCTCTCTTCTGTAAAGGATTG 118
Qy 353 CCTTCTGTTTTAGAGAGACTAAACAGACATTTGAAAGTTCAGGTAAAGCTGAATATAAC 412
Db 119 CCTTCTTGAATAGAGAGATTAGACAGACGTGGAGAG-----CACCCTGAAGTTACC 170
Qy 413 ATTGCTGAATGTTTTTCC--TTGTGTATTTTAAAGGCTGAGACATTTATCGAGAAAG 470
Db 171 ATTGCTGAATGTTTTTCCCTATGTGTATTTTAAAGGACCAAGACACTATCGAGAAAG 230
Qy 471 ACTGGATATATCATAGAGGAAAGAACTGTTCCA 506
Db 231 GCTGGAATAACCAAGAAAGAAAGAACTGTTCCA 266

RESULT 13
BD094780 636 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION
The cell having the potentiality of differentiation into
cardiomyocytes.
ACCESSION
BD094780
VERSION
BD094780.1 GI:22640368
KEYWORDS
WO 0148150-A/47,
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 636)
AUTHORS
Umezawa, A., Hata, J., Fukuda, K., Ogawa, S., Sakurada, K., Gojo, S. and
Yamada, Y.
TITLE
The cell having the potentiality of differentiation into
JOURNAL
PATENT: WO 0148150-A 47 05-JUL-2001;
KYOWA HAKKO KOGYO CO LTD, AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI
FUKUDA, SATOSHI OGAWA, KAZUHIRO SAKURADA, SATOSHI GOJO, YOI YAMADA
COMMENT
OS Homo sapiens (human)
PN WO 0148150-A/47
PD 05-JUL-2001
PF 02-NOV-2000 WO 2000JP007741
PR 28-DEC-1999 JP 99P 372826, 28-FEB-2000 WO PCTJP0001448 PI
AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI FUKUDA, SATOSHI OGAWA, PI
KAZUHIRO SAKURADA, SATOSHI GOJO, YOI YAMADA
PC C12N5/06, C12N5/10, C12N15/09, A61K31/203, A61K35/28, A61K38/19, PC
A61K38/39,
PC A61K38/45, A61K48/00, A61P9/10, A61P41/00, C07K16/28, C12P21/08, PC
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PC C12Q1/48, G01N33/577
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FT CDS Location/Qualifiers
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Qy 128 GCACGTTGTTCCGTATGGACTTCGAAGCCCTAGGTCCAAGAGAGCCTTGAGAAATTACT 187
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Db 294 TCCCAACAAGGCAACAGACCGTGAATATAGATCCCAATGTGCTAGCCAAAAGACAGAA 353
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QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACAGAAA 294
DB 354 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACAGAAA 400

RESULT 14
LOCUS BD096322 636 bp DNA linear PAT 27-AUG-2002
DEFINITION Cells capable of differentiating into myocardial cells.
ACCESSION BD096322
VERSION BD096322.1 GI:22641910
KEYWORDS WO 0148151-A/47.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 636)
AUTHORS Umezawa,A., Hata,J., Fukuda,K., Ogawa,S., Sakurada,K., Gojo,S. and Yamada,Y.
TITLE Cells capable of differentiating into myocardial cells
JOURNAL Patent: WO 0148151-A 47 05-JUL-2001;
KYOWA HAKKO KOGYO CO LTD
COMMENT OS Homo sapiens (human)
PN WO 0148151-A/47
PD 05-JUL-2001
PF 27-DEC-2000 WO 2000JP009323
PR 28-DEC-1999 JP 99P 372826, 28-FEB-2000 WO PCTJP0001148 PR
O2-NOV-2000 WO PCTJP0007741
PI AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI FUKUDA, SATOSHI OGAWA, PI
KAZUHIRO SAKURADA, SATOSHI GOJO, YOJI YAMADA
PC C12N5/06, C12N5/08, C12P21/08, C12Q1/02, A61K35/28, A61K35/44, A61P9/ PC
06,
PC A61P9/04//A61K38/18, C12N15/12
CC Cells capable of differentiating into myocardial cells FH
Key Location/Qualifiers
FT CDS (1)..(639).

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ORIGIN
Query Match 6.8%; Score 157.4; DB 6; Length 636;
Best Local Similarity 96.4%; Pred. No. 4.7e-25;
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 GCACGTGTTCCGTATGCACTTGGAGCCCTAGGTCCAGAGAGCCTTGGAGATTACT 187
DB 234 GCACGTGTTCCGTATGCACTTGGAGCCCTAGGTCCAGAGAGCCTTGGAGATTACT 293
QY 188 TCCCAAGAGGCAACAGACCGGTGAGATAGATGCCAATGTGCTAGCCAAAAGCAAGAA 247
DB 294 TCCCAAGAGGCAACAGACCGGTGAGATAGATGCCAATGTGCTAGCCAAAAGCAAGAA 353
QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACAGAAA 294
DB 354 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACAGAAA 400

RESULT 15
LOCUS HSET 1167 bp mRNA linear PRI 23-MAR-1995
DEFINITION Human mRNA for endothelin.
ACCESSION Y00749
VERSION Y00749.1 GI:31254
KEYWORDS endothelin; vasoconstrictor peptide.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1167)

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AUTHORS Itoh,Y., Yanagisawa,M., Ohkubo,S., Kimura,C., Kosaka,T., Inoue,A.,
Ishida,N., Mitsui,Y., Onda,H., Fujino,M. and Masaki,T.
TITLE Cloning and sequence analysis of cDNA encoding the precursor of a
human endothelium-derived vasoconstrictor peptide, endothelin:
identity of human and porcine endothelin
FEBS Lett. 231 (2), 440-444 (1988)
JOURNAL MEDLINE 88196441
PUBMED 3282927
REFERENCE 2 (bases 1 to 1167)
AUTHORS Itoh,Y.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1988) Itoh Y., Wadai 7, Tsukuba, Ibaraki 300-42,
Japan
COMMENT Data kindly reviewed (01-JUN-1988) by Itoh Y.
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253..891
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/db_xref="GOA:P05305"
/db_xref="SWISS-PROT:P05305"
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mat_peptide 409..471
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/product="mature endothelin (AA 36 - 56)"

ORIGIN
Query Match 6.8%; Score 157.4; DB 9; Length 1167;
Best Local Similarity 96.4%; Pred. No. 4.5e-25;
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 GCACGTGTTCCGTATGCACTTGGAGCCCTAGGTCCAGAGAGCCTTGGAGATTACT 187
DB 486 GCACGTGTTCCGTATGCACTTGGAGCCCTAGGTCCAGAGAGCCTTGGAGATTACT 545
QY 188 TCCCAAGAGGCAACAGACCGGTGAGATAGATGCCAATGTGCTAGCCAAAAGCAAGAA 247
DB 546 TCCCAAGAGGCAACAGACCGGTGAGATAGATGCCAATGTGCTAGCCAAAAGCAAGAA 605
QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACAGAAA 294
DB 606 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACAGAAA 652

Search completed: July 16, 2004, 20:03:52
Job time : 8815 secs

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4	2241.6	97.4	12461	3	AAF21289		AAF21289 Human low
5	2241.6	97.4	12461	6	ABK83778		ABK83778 Human cdn
6	2241.6	97.4	12461	7	ABF296983		ABF296983 Human nuc
7	2241.6	97.4	12461	7	ACA64929		ACA64929 Human bdn
8	2241.6	97.4	14879	3	Aax35170		Aax35170 Human ade
9	2241.6	97.4	14879	3	AAF21292		AAF21292 Human low
10	2241.6	97.4	14879	7	AB296986		AB296986 Human nuc
11	2239.6	97.3	12459	6	AB280449		AB280449 Human end
12	1559	6.9	1250	7	ABV76130		ABV76130 Human end
13	157.4	6.8	636	4	Aah48266		Aah48266 Heart mus
14	157.4	6.8	636	4	Aah44397		Aah44397 Human Etl
15	157.4	6.8	1167	3	AA35169		AA35169 Human ade
16	157.4	6.8	1167	3	AAF21291		AAF21291 Human low
17	157.4	6.8	1167	3	AA354135		AA354135 Preproend
18	157.4	6.8	1167	7	AB296985		AB296985 Human nuc
19	157.4	6.8	1175	1	AAN90770		AAN90770 Human end
20	157.4	6.8	1175	1	AAN90721		AAN90721 Human end
21	157.4	6.8	1251	3	AA35168		AA35168 Human ade
22	157.4	6.8	1251	3	AAF21290		AAF21290 Human low
23	157.4	6.8	1251	6	AB234493		AB234493 Human cen

CC for a particular therapy to treat a vascular disease or disorder  
 CC comprises determining the presence of nucleotides at polymorphic regions  
 CC of an endothelin-1 (EDN1) gene. The invention is used to determine risk  
 CC of developing a vascular disease or disorder, particularly coronary  
 CC artery disease or myocardial infarction. The present sequence represents  
 CC the human endothelin-1 gene.  
 XX

QY Sequence 186510 BP; 56192 A; 36427 C; 37117 G; 56774 T; 0 U; 0 Other;

QY	1	CTGAATGATGCTCCCAAGTCTATGTGATGAGTCTCTGTGTCGCCAGTGGAAATAGGTG	60
DB	157700	CTGAATGATGCTCCCAAGTCTATGTGATGAGTCTCTGTGTCGCCAGTGGAAATAGGTG	157759
QY	61	TGTCATGTCGATTTAAAGACTATTAAATACACTAATAGTTTCTTCTCTCTTTGG	120
DB	157760	TGTCATGTCGATTTAAAGACTATTAAATACACTAATAGTTTCTTCTCTCTTTGG	157819
QY	121	ATAATAGGACAGTTCTTCCGTATGGACTTGGAGCCCTAGGTCCAGAGAGCCCTTGGAGA	180
DB	157820	ATAATAGGACAGTTCTTCCGTATGGACTTGGAGCCCTAGGTCCAGAGAGCCCTTGGAGA	157879
QY	181	ATTACTTCCCAAGGCAACAGACCTGAAATAGATGCAATGTGCTAGCCAAAAG	240
DB	157880	ATTACTTCCCAAGGCAACAGACCTGAAATAGATGCAATGTGCTAGCCAAAAG	157939
QY	241	ACAGAAGTGTGGAAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT	300
DB	157940	ACAGAAGTGTGGAAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT	157999
QY	301	TGCTTTTCAATCAGTTTAAAGCCCTCTGAACTCTCTCTCTCTCTCTCTCTCTCTG	360
DB	158000	TGCTTTTCAATCAGTTTAAAGCCCTCTGAACTCTCTCTCTCTCTCTCTCTCTCTG	158059
QY	361	TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGTGAAAGTCAATATACATTTGCTGA	420
DB	158060	TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGTGAAAGTCAATATACATTTGCTGA	158119
QY	421	AATGTTTTTCCCTGTTATTTTAAAGGCTGAGACATTTATGAGAAAGCTGGAATAA	480
DB	158120	AATGTTTTTCCCTGTTATTTTAAAGGCTGAGACATTTATGAGAAAGCTGGAATAA	158179
QY	481	TCATAGAGAAAGAAAGACTGTTTCAAGCTTGGGAAAGTGTATTTATCAGCAGTTAGT	540
DB	158180	TCATAGAGAAAGAAAGACTGTTTCAAGCTTGGGAAAGTGTATTTATCAGCAGTTAGT	158239
QY	541	GAGAGAAAGAAATCAGAAGAGTTTCAGAGAAACCTTAAGACAAACACAGGTAAAGAGG	600
DB	158240	GAGAGAAAGAAATCAGAAGAGTTTCAGAGAAACCTTAAGACAAACACAGGTAAAGAGG	158299
QY	601	AGGAGAAAGAAATTAGGTAAAGGTTTCAAGACAACTAGCCCAAGTCAGTGATGCCAG	660
DB	158300	AGGAGAAAGAAATTAGGTAAAGGTTTCAAGACAACTAGCCCAAGTCAGTGATGCCAG	158359
QY	661	CAGCCTGTTCTTCCAGCCCTTCTTACCCTGAGGTGAAAGACTTAGAAGAAACAGTAGCAG	720
DB	158360	CAGCCTGTTCTTCCAGCCCTTCTTACCCTGAGGTGAAAGACTTAGAAGAAACAGTAGCAG	158419
QY	721	AGGAGATCTATGATCTTATAGATTTAAAGAGGCAAGAAATCCCTCTTAATATTTCCA	780
DB	158420	AGGAGATCTATGATCTTATAGATTTAAAGAGGCAAGAAATCCCTCTTAATATTTCCA	158479
QY	781	TGAAGCTCTGGAATGCAAAACCAATGTCCTCTGTACTTTTAGCACATACCATTTCTATC	840
DB	158480	TGAAGCTCTGGAATGCAAAACCAATGTCCTCTGTACTTTTAGCACATACCATTTCTATC	158539
QY	841	AGGTAGATTTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCTATTTGGTTATATACG	900
DB	158540	AGGTAGATTTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCTATTTGGTTATATACG	158599

QY	901	CTTTGCCCTCTGAGTCAATGATTTTACACTTTCCCTGAGAAATCGAAATCATTTTGG	960
DB	158600	CTTTGCCCTCTGAGTCAATGATTTTACACTTTCCCTGAGAAATCGAAATCATTTTGG	158659
QY	961	GGAGGGGACATTTAGAAAAAGAAATCAAAAGTGTGATGGATAATCAAAATCTTCAATAGTT	1020
DB	158660	GGAGGGGACATTTAGAAAAAGAAATCAAAAGTGTGATGGATAATCAAAATCTTCAATAGTT	158719
QY	1021	GCAGTTATTTCAGATGCGCAAGAAAAATAAGTCAATAGATAGGTTGGTAGAATTTAG	1080
DB	158720	GCAGTTATTTCAGATGCGCAAGAAAAATAAGTCAATAGATAGGTTGGTAGAATTTAG	158779
QY	1081	AACATGCTGTTTTTTCAGGTTTATGCTCTTTTTTTTTTTTTTTTTTTTTTAAATAGGAAATG	1140
DB	158780	AACATGCTGTTTTTTCAGGTTTATGCTCTTTTTTTTTTTTTTTTTTTTTTAAATAGGAAATG	158839
QY	1141	TGTTGGTGCAGAGCAATGTCAATCCAAAAGCTCTCTTTTTCTCGTCAGTCAATGTG	1200
DB	158840	TGTTGGTGCAGAGCAATGTCAATCCAAAAGCTCTCTTTTTCTCGTCAGTCAATGTG	158899
QY	1201	CTGGACAGAGAGAGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGTCTCTTT	1260
DB	158900	CTGGACAGAGAGAGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGTCTCTTT	158959
QY	1261	GGTGATAAACCCCTTCCAAATCTTAAACTTTTGGAAATTCACAAAGCTCAAAAGGAGAAACCT	1320
DB	158960	GGTGATAAACCCCTTCCAAATCTTAAACTTTTGGAAATTCACAAAGCTCAAAAGGAGAAACCT	159019
QY	1321	ACTCTGATCTACACATGTTCTGCATTTTCTATCATGCTCTATGGAATCTCTCTTA	1380
DB	159020	ACTCTGATCTACACATGTTCTGCATTTTCTATCATGCTCTATGGAATCTCTCTTA	159079
QY	1381	GAAATCCAGTGGCAAGAGTCTTATGATTAAAGTGTCTGAGCTCAGGCCAGGAGTCAAT	1440
DB	159080	GAAATCCAGTGGCAAGAGTCTTATGATTAAAGTGTCTGAGCTCAGGCCAGGAGTCAAT	159139
QY	1441	GAACTACTTCTGAGTTATTACTGATTTGTTGGGGAGCCCTCAGCTATCGGTTTCTTTC	1500
DB	159140	GAACTACTTCTGAGTTATTACTGATTTGTTGGGGAGCCCTCAGCTATCGGTTTCTTTC	159199
QY	1501	ACACCTGCTTATGAGAGTATCCATATTTATGTTCCAGCCAGTAAATGCTCCCCACGAGA	1560
DB	159200	ACACCTGCTTATGAGAGTATCCATATTTATGTTCCAGCCAGTAAATGCTCCCCACGAGA	159259
QY	1561	TCAGTTTCTGAACTAACCTGGAAATTTTATGAGTTTATATGCTTAACTTAAATCA	1620
DB	159260	TCAGTTTCTGAACTAACCTGGAAATTTTATGAGTTTATATGCTTAACTTAAATCA	159319
QY	1621	ACATTCAGTTTCTCCCTCTGATTTCTCCTGTAACCAATAGGCTCGCAAAAAAATAA	1680
DB	159320	ACATTCAGTTTCTCCCTCTGATTTCTCCTGTAACCAATAGGCTCGCAAAAAAATAA	159379
QY	1681	ATCTTTTAAAAAATAATGCCATAAAGTATTTGCTCTGGGCTCTGATGCTCTTTTC	1740
DB	159380	ATCTTTTAAAAAATAATGCCATAAAGTATTTGCTCTGGGCTCTGATGCTCTTTTC	159439
QY	1741	TTTTTCTCTCTTTTCACTAAGTCCCGTCAATTTTAAAGATGCCATACTATTTCAA	1800
DB	159440	TTTTTCTCTCTTTTCACTAAGTCCCGTCAATTTTAAAGATGCCATACTATTTCAA	159499
QY	1801	ACCTATGCTGAGTTCTCAGGACAGGTCACATAGTATGATGAAAGTTGGGATGGGCTAGC	1860
DB	159500	ACCTATGCTGAGTTCTCAGGACAGGTCACATAGTATGATGAAAGTTGGGATGGGCTAGC	159559
QY	1861	GAAGAAACAGAACTCTAGTTTATTTAAACCTGATTTTACTGCCACCTTCCCTTA	1920
DB	159560	GAAGAAACAGAACTCTAGTTTATTTAAACCTGATTTTACTGCCACCTTCCCTTA	159619
QY	1921	GACTTCCACCATATGACCCCTCGCTCCATTCTTAAGCATAGGGGAGGCTTTATTTTACA	1980
DB	159620	GACTTCCACCATATGACCCCTCGCTCCATTCTTAAGCATAGGGGAGGCTTTATTTTACA	159679
QY	1981	ATGGTAATAGATATCACTTGAGGTTTTTATCAAGAGTTCGCGGGGTGGTGAAGTTTAC	2040

||||| 159680 ATGGTAATAGATATCACATTGAGTTTATCAAGAGTTTGGCGGGTGGTGAAGTTTCAC 159739  
QY 2041 AACGAGATTCAGGTTTGTGTCAGATCTTAATTTACATGTTCTTTTGCAGAGG 2100  
DB 159740 AACGAGATTCAGGTTTGTGTCAGATCTTAATTTACATGTTCTTTTGCAGAGG 159799  
QY 2101 GTGATTTTAAATAACATTTGTTTCTCTTATCTGCTTTTATAGTTCGAGAGCCAT 2160  
DB 159800 GTGATTTTAAATAACATTTGTTTCTCTTATCTGCTTTTATAGTTCGAGAGCCAT 159859  
QY 2161 GAGAAACAGGTCATATCTTTTCATGATCCCAAGCTGAAGGAGCCCTCCAGAGA 2220  
DB 159860 GAGAAACAGGTCATATCTTTTCATGATCCCAAGCTGAAGGAGCCCTCCAGAGA 159919  
QY 2221 GGGTTATGTGACCCCAACCCGAGACATTTGTTGACAGACCTTCGGGGCTGCTGAAGCC 2280  
DB 159920 GGGTTATGTGACCCCAACCCGAGACATTTGTTGACAGACCTTCGGGGCTGCTGAAGCC 159979  
QY 2281 ATAGCCTCCAGGAGAGCCCT 2301  
DB 159980 ATAGCCTCCAGGAGAGCCCT 160000  
  
RESULT 2  
ID AAX32367  
XX AAX32367 standard; DNA; 12461 BP.  
XX AC AAX32367;  
XX AC AAX32367;  
DT 16-JUN-1999 (first entry)  
XX Human endothelin-1 (ET-1) gene sequence.  
DE Human endothelin-1 (ET-1) gene sequence.  
KW Pulmonary hypertension; therapeutic; aerosolized; endothelin-1; ET-1;  
KW lung; antisense; ss.  
XX Homo sapiens.  
XX WO9911778-A1.  
XX 11-MAR-1999.  
XX 02-SEP-1998; 98WO-GB002584.  
XX 02-SEP-1997; 97GB-00018487.  
XX (UYSH-) UNIV SHEFFIELD.  
XX Higenbottam T, McCormack K, Smith A;  
XX WPI; 1999-205185/17.  
XX New composition containing an aerosolized antisense ET-1 molecule -  
XX useful for treating pulmonary hypertension.  
XX Disclosure; Fig.1; 37pp; English.  
XX The invention relates to a method for treating pulmonary hypertension by  
XX delivering a therapeutic composition, comprising an aerosolized antisense  
XX endothelin-1 (ET-1) molecule, to the lungs of a patient. The composition  
XX can be used in a method for determining the efficacy of the treatment for  
XX e.g. when studying molecules and observing the effects of the composition  
XX on an animal model system hypersensitive to antisense ET-1. The method is  
XX useful for treating pulmonary hypertension. The aerosolized antisense ET-  
XX 1 molecule permits inhibition of the ET-1 transcription, which relieves  
XX pulmonary hypertension. Its use avoids side effects caused by alternative  
XX therapies. The present sequence represents the genomic DNA sequence of  
XX human ET-1 gene  
SQ Sequence 12461 BP; 3372 A; 2728 C; 2816 G; 3544 T; 0 U; 1 Other;  
Query Match 97.4%; Score 2241.6; DB 2; Length 12461;

Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2294; Conservative 1; Mismatches 5; Indels 10; Gaps 4;  
QY 1 CTGAATATGATGCTCCCAAGTCTATGTGATGAGCTCCCTTGTGTCGCCAGTGAATAGGTG 60  
DB 7056 CTGAATATGATGCTCCCAAGTCTATGTGATGAGCTCCCTTGTGTCGCCAGTGAATAGGTG 7115  
QY 61 TGTCCATGTGTCATTTTAAAGACTATTAATTAACACTAATATAGTTTCTTTCTCTTTGG 120  
DB 7116 TGTCCATGTGTCATTTTAAAGACTATTAATTAACACTAATATAGTTTCTTTCTCTTTGG 7175  
QY 121 ATAAATAGGACAGTGTTCGATGAGACTTTGGAAGCCCTAGGTCCAAAGAGAGCCCTTGGAGA 180  
DB 7176 ATAAATAGGACAGTGTTCGATGAGACTTTGGAAGCCCTAGGTCCAAAGAGAGCCCTTGGAGA 7235  
QY 181 ATTTTACTTCCCAAGAGGCAACAGACCGTGAAAAATAGATGCCAATGTGTAGTCCAAAAAG 240  
DB 7236 ATTTTACTTCCCAAGAGGCAACAGACCGTGGAATAGATGCCAATGTGTAGTCCAAAAAG 7295  
QY 241 ACAAGAAGTGTGGAATTTTTCGCAAGCAGGAAAAAGAACTCAGGTGAGCAGAAAAACCTTT 300  
DB 7296 ACAAGAAGTGTGGAATTTTTCGCAAGCAGGAAAAAGAACTCAGGTGAGCAGAAAAACCTTT 7355  
QY 301 TGCCTTTCAATCAGTTTAAAGCCTCTGAACTCCCTTCCCTATCATGTGTTACTGCTTCCTG 360  
DB 7356 TGCCTTTCAATCAGTTTAAAGCCTCTGAACTCCCTTCCCTATCATGTGTTACTGCTTCCTG 7415  
QY 361 TTTTACAGAGACTAACAGAGACATTTGAAAGTCAAGGTAAAGCTGAATATAAATTTGCTGA 420  
DB 7416 TTTTACAGAGACTAACAGAGACATTTGAAAGTCAAGGTAAAGCTGAATATAAATTTGCTGA 7475  
QY 421 AATGTTTTTCCCTGTGTATTTTAAAGGCTGAAGACATTTGGAGAAAGACTGGAAATAA 480  
DB 7476 AATGTTTTTCCCTGTGTATTTTAAAGGCTGAAGACATTTGGAGAAAGACTGGAAATAA 7535  
QY 481 TCATAAGAAAGGAAAAAGACTGTTTCCAAAGCTTGGAAAAAGTGTATTATCAGCAGTTAGT 540  
DB 7536 TCATAAGAAAGGAAAAAGACTGTTTCCAAAGCTTGGAAAAAGTGTATTATCAGCAGTTAGT 7595  
QY 541 GAGAGAAAGAAAAATCAGAAAGTTTCAAGAGGCAACCTTAAGACAAACAGAGTAAGAGGG 600  
DB 7596 GAGAGAAAGAAAAATCAGAAAGTTTCAAGAGGCAACCTTAAGACAAACAGAGTAAGAGGG 7655  
QY 601 AAGGAAAGAAAAATTAGTAAAGGTTTCAAGAAACAACTAGCCCACTCAGTGAATGCCAG 660  
DB 7656 AAGGAAAGAAAAATTAGTAAAGGTTTCAAGAAACAACTAGCCCACTCAGTGAATGCCAG 7715  
QY 661 CAGCCTGTTTCTCCAGCCCTTCTTACCCTGGGAGGTGAAGACTTAGAAAAACAGTAGCAG 720  
DB 7716 CAGCCTGTTTCTCCAGCCCTTCTTACCCTGGGAGGTGAAGACTTAGAAAAACAGTAGCAG 7775  
QY 721 AGGAGATCTATGATCCTATAGATTTAAAGGAGCAAAAGAAATCCCTCTTAAATATTTCCA 780  
DB 7776 AGGAGATCTATGATCCTATAGATTTAAAGGAGCAAAAGAAATCCCTCTTAAATATTTCCA 7835  
QY 781 TGAAGCTCTGGAATGCAAAACCGATGCTCTGTACTTTTAGCACAATCCATTTTCACTAC 840  
DB 7836 TGAAGCTCTGGAATGCAAAACCGATGCTCTGTACTTTTAGCACAATCCATTTTCACTAC 7895  
QY 841 AGTGAATTTCCCAACCAAAATATATCCAGAGATGCTTTGTTCATTTGGGTTATATACAG 900  
DB 7896 AGTGAATTTCCCAACCAAAATATATCCAGAGATGCTTTGTTCATTTGGGTTATATACAG 7955  
QY 901 CTTTGGCTCTCTGAGTCAATGTATTTTACCCTTTCCCTCAGAAATCGAAATCATTTTGG 960  
DB 7956 CTTTGGCTCTCTGAGTCAATGTATTTTACCCTTTCCCTCAGAAATCGAAATCATTTTGG 8015  
QY 961 GGAGCGGACATTTAGAAAAAGAAATCAAGTGTATGGAATAATCAAAATTTCTCAATAAGTT 1020  
DB 8016 GGAGCGGACATTTAGAAAAAGAAATCAAGTGTATGGAATAATCAAAATTTCTCAATAAGTT 8075  
QY 1021 GCAGTTATTTCAGATGGCCAAAGGAAAAATAAAGTCAATAGATAGGTTTGGTAGAATTAG 1080

8076 GCAGTTATTCAGATGGCCAAAGGAAATAAAGTCATTAGATAGGTTGGTGAATTTAG 8135  
1081 AACATGCTGTTTTCAGGTTTATGGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 1135  
8136 AACATGCTGTTTTCAGGTTTATGGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 8195  
1136 AAATGTTTGGTGAGAGCCAAATGTCATTCAAAAAGCTCTCTCTTTTCTGTCAGTC 1195  
8196 AAATGTTTGGTGAGAGCCAAATGTCATTCAAAAAGCTCTCTCTTTTCTGTCAGTC 8255  
1196 ATGTCCTGGGACAGAGAGGATCTGGATTAGGCAACATCATAGATTGCTCTCAGCTGC 1255  
8256 ATGTCCTGGGACAGAGAGGATCTGGATTAGGCAACATCATAGATTGCTCTCAGCTGC 8315  
1256 TCTTTGGTGATAACCCCTTCCAAATCCTAAACCTTTTGGAAATCAAGCTCAAAAGGAGGA 1315  
8316 TCTTTGGTGATAACCCCTTCCAAATCCTAAACCTTTTGGAAATCAAGCTCAAAAGGAGGA 8375  
1316 AACCTACTCTCTGATCTACCAATGTTCTGCAATTTTCTATCATGCTATGGAACCTTC 1375  
8376 AACCTACTCTCTGATCTACCAATGTTCTGCAATTTTCTATCATGCTATGGAACCTTC 8435  
1376 TCTTAGAAATCCAGTGGCAAGAGTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 1435  
8436 TCTTAGAAATCCAGTGGCAAGAGTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 8495  
1436 GTCATGAATCTCTGATCTAGTTATTTACTACTGATTTTGGGGAGCTCAGCTATCGTT 1495  
8496 GTCATGAATCTCTGATCTAGTTATTTACTACTGATTTTGGGGAGCTCAGCTATCGTT 8555  
1496 TCTTCACACCTGCTTATGAGAGTATCCATATTTATGTCGAGCCAGTATGCTCCCCA 1555  
8556 TCTTCACACCTGCTTATGAGAGTATCCATATTTATGTCGAGG-CAGTATGCTCCCA 8614  
1556 CGAGATCAGTTCTGAACTAACCTGGAAATTTTATGAGGTTTATTAAGCCAACTATTA 1615  
8615 CGAGATCAGTTCTGAACTAACCTGGAAATTTTATGAGGTTTATTAAGCCAACTATTA 8674  
1616 AATCAACATTCAGTTCTTCCCTCTGATTTCTCTCTGTAACATTTAGGCTCGAAAAA 1675  
8675 AATCAACATTCAGTTCTTCCCTCTGATTTCTCTCTGTAACATTTAGGCTCGAAAAA 8734  
1676 AAAAAATCTTTTAAAAATAATGCAATAAGTATTTGCTCTGGCCCTACTGATGCTTC 1735  
8735 AAAAAATCTTTTAAAAATAATGCAATAAGTATTTGCTCTGGCCCTACTGATGCTTC 8794  
1736 TTTTCTTTTCTCTCTCTTCTCACTAAGTCACCGTCATTTATTAAGATGGCCATAACTAT 1795  
8795 TTTTCTTTTCTCTCTCTTCTCACTAAGTCACCGTCATTTATTAAGATGGCCATAACTAT 8854  
1796 TCAAAACCTATGCTGAGTTCCTCAAGGAGGCTCACAATGATGATCAAGGTTGGGATGGG 1855  
8855 TCAAAACCTATGCTGAGTTCCTCAAGGAGGCTCACAATGATGATCAAGGTTGGGATGGG 8914  
1856 CTACGGAGAGACACAGAACCTCTAGTTTATTTAAACCTGTATTTACTGCCCACTTCC 1915  
8915 CTACGGAGAGACACAGAACCTCTAGTTTATTTAAACCTGTATTTACTGCCCACTTCC 8974  
1916 CTTAGACTTGACCATATGACCCCTGCT-CCCATTTCAAGCATAGGGGAGGCTTTATT 1974  
8975 CTTAGACTTGACCATATGACCCCTGCTCCCATTTCAAGCATAGGGGAGGCTTTATT 9034  
1975 TTTAATGTTAATA---GATATCACTTGAAGTTTATCAAGATGTCGGCGGGTGGTG 2031  
9035 TTTAATGTTAATAAGATGATACATCTGAGGTTTATCAAGAGTTGCGCGGGTGGTG 9094  
2032 AAAGTTCAACACGATTCAGGTTTGTGTCGAGATTCCTAATTTTACATGTTCTTT 2091  
9095 AAAGTTCAACACGATTCAGGTTTGTGTCGAGATTCCTAATTTTACATGTTCTTT 9154  
2092 TGCCAAAGGGTGAATTTTTTAAATAACATTTGTTTCTCTTATCTGCTTTATAGGTC 2151  
9155 TGCCAAAGGGTGAATTTTTTAAATAACATTTGTTTCTCTTATCTGCTTTATAGGTC 9214

2152 GGAGACCATGAGAAAACAGCGTCAAAATCATCTTTTTCATGCCAAGCTGAAAGGCAAGCC 2211  
9215 GGAGACCATGAGAAAACAGCGTCAAAATCATCTTTTTCATGCCAAGCTGAAAGGCAAGCC 9274  
2212 CTCACAGAGCGTTTATGTGACCCCAACCGAGCACATTTGGTGACAGACCTTCGGGGCCCTG 2271  
9275 CTCACAGAGCGTTTATGTGACCCCAACCGAGCACATTTGGTGACAGACCTTCGGGGCCCTG 9334  
2272 TCTGAAGCCATAGCCTCCACGAGAGCCCT 2301  
9335 TCTGAAGCCATAGCCTCCACGAGAGCCCT 9364

## RESULT 3

AAA35167

ID AAA35167 standard; DNA; 12461 BP.

XX AAA35167;

AC AAA35167;

XX 28-JUL-2000 (first entry)

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:41.

XX

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiasthmatic; cyostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200009525-A2.

FN 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

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Disclosure; Page 1198-1201; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cyostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the



QY	1975	TTTCAATAGCGTAATA---GATATCACCTTGAGGTGTTTATCAAGAGTTGCGCGGGTGCTG	2031
Db	9035	TTTACAAATGGTAATGATGATATCACCTTGAGGTGTTTATCAAGAGTTGCGCGGGTGCTG	9094
QY	2032	AAAGTTCAACAACAGATTCAGGTTTGTGTCACAGATTCTAATTTTACATGTTCTTTT	2091
Db	9095	AAAGTTTCACAACAGATTCAGGTTTGTGTCACAGATTCTAATTTTACATGTTCTTTT	9154
QY	2092	TGCCAAAGGCTGATTTTTTAAATAACATTGTTTTCTCTTATCTTGCTTTTATTAGGTC	2151
Db	9155	TGCCAAAGGCTGATTTTTTAAATAACATTGTTTTCTCTTATCTTGCTTTTATTAGGTC	9214
QY	2152	GGAGACCATGAGAAACAGCGTCAAAATCATCTTTTCATGATCCCAAGCTGAAGGCAAGCC	2211
Db	9215	GGAGACCATGAGAAACAGCGTCAAAATCATCTTTTCATGATCCCAAGCTGAAGGCAAGCC	9274
QY	2212	CTCCAGAGACGCTTATGTGACCCACACACCGAGACACATTTGGTGTACAGACCTTCCTGGGGCCTG	2271
Db	9275	CTCCAGAGACGCTTATGTGACCCACACACCGAGACACATTTGGTGTACAGACCTTCCTGGGGCCTG	9334
QY	2272	TCTGAAGCCATAGCCTCCACGGAGAGCCCT	2301
Db	9335	TCTGAAGCCATAGCCTCCACGGAGAGCCCT	9364
RESULT 4			
AAF21289			
ID	AAF21289 standard; DNA; 12461 BP.		
XX			
AC	AAF21289;		
XX			
DT	14-MAR-2001 (first entry)		
XX			
DE	Human low adenosine antisense oligonucleotide related sequence #2856.		

(I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiaesthetic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypo-production which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR1543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

SX Sequence 12461 BP; 3372 A; 2728 C; 2816 G; 3544 T; 0 U; 1 Other;

	Query Match Best Local Similarity Matches 2294; Conservative	97.4%; 99.3%;	Score 2241.6; Pred. No. 0;	DB 3;	Length 12461;	Mismatches 1;	Gaps 4;
QY	1	CTGAATGATGTCTCCCAAGTCTATGTGATGAGCTCCTTGTCGCCACGTGGAATAGGTTG	60				
Db	7056	CTGAATGATGTCTCCCAAGTCTATGTGATGAGCTCCTTGTCGCCACGTGGAATAGGTTG	7115				
QY	61	TGTCGAATGTGCATTTTAAAGACTATTAAATTACATAATATAGTTCTTTCTCTCTTTGG	120				
Db	7116	TGTCCAATGTGCATTTTAAAGACTATTAAATTACATAATATAGTTCTTTCTCTCTTTGG	7175				
QY	121	ATAATAGGACGCTGTGTCGATGGACCTTGGAAAGCCCTAGGTCCTAAGAGAGCGCTTGGAGA	180				
Db	7176	ATAATAGGACGCTGTGTCGATGGACCTTGGAAAGCCCTAGGTCCTAAGAGAGCGCTTGGAGA	7235				
QY	181	ATTACTTCCCACAAAGGCAACAGACCGTGAAATATAGATGCCAATGTGCTAGCCAAAAG	240				
Db	7236	ATTACTTCCCACAAAGGCAACAGACCGTGAAATATAGATGCCAATGTGCTAGCCAAAAG	7295				
QY	241	ACAAGAAGTGTCTGGAAATTTTTCGCAAGCAGGAGAAAGAACTCAGGTCAGCAGAAAAACCTT	300				
Db	7296	ACAAGAAGTGTCTGGAAATTTTTCGCAAGCAGGAGAAAGAACTCAGGTCAGCAGAAAAACCTT	7355				
QY	301	TGCTTTTCAATCAGTTTTAACAGCCTCTCGAATCTCTTCCATCATGTGTACTGCTCTCTG	360				
Db	7356	TGCTTTTCAATCAGTTTTAACAGCCTCTCTGAACTCTCTTCAATGTGTACTGCTCTCTG	7415				
QY	361	TTTTTAGAGAGACTAACACAGAGACATTTGAAAGTCAGGTAAGCTGAATATAACATTGCTGA	420				
Db	7416	TTTTTAGAGAGACTAACACAGAGACATTTGAAAGTCAGGTAAGCTGAATATAACATTGCTGA	7475				
QY	421	AATGTTTTTCTTGTGTATTTTAAACAGGCTGGAACATTTATGGAGAAAGACTGGAATTA	480				
Db	7476	AATGTTTTTCTTGTGTATTTTAAACAGGCTGGAACATTTATGGAGAAAGACTGGAATTA	7535				
QY	481	TCATAAGAAAGCAAAGACTGTTTCCAAGCTTCGGGAAAAAGTCTATTATCACAGTTAGT	540				
Db	7536	TCATAAGAAAGCAAAGACTGTTTCCAAGCTTCGGGAAAAAGTCTATTATCACAGTTAGT	7595				
QY	541	GAGAGAGAAAAAATTCAGAAGATTTTCAGAGGAAACCTCTAAGACAAAACGAGTTAAGGG	600				
Db	7596	GAGAGAGAAAAAATTCAGAAGATTTTCAGAGGAAACCTCTAAGACAAAACGAGTTAAGGG	7655				

Db	8735	AAAAATCTTTTAAAAATAATGGCATAAAGATATTTGCTCTGGGCTACTGATGCTTC	8794
Qy	1736	TTTTCTTTTCTCTCTTTTCAACTAAGTCACCGTCAATTTATTAGATGGCCATAACTAT	1795
Db	8795	TTTTVTTTTTCTCTCTTTTCAACTAAGTCACCGTCAATTTATTAGATGGCCATAACTAT	8854
Qy	1796	TCAAAACCTATGCTGAGTTGCTTCAAGGACGGGTGCATAGTGATGAAGTGGGATGGG	1855
Db	8855	TCAAAACCTATGCTGAGTTGCTTCAAGGACGGGTGCATAGTGATGAAGTGGGATGGG	8914
Qy	1856	CTACGGAAGAACCGAACAACCTCTAGTTTATTAAACCTGTATTTACTTGCCCACTTC	1915
Db	8915	CTACGGAAGAACCGAACAACCTCTAGTTTATTAAACCTGTATTTACTTGCCCACTTC	8974
Qy	1916	CTTTAGACATTGACCATATAGACCCCTCGCT-CCCATCTAAGCATAGGGCAGGCTTTATT	1974
Db	8975	CTTTAGACATTGACCATATAGACCCCTCGCTCCCATTTCTAAGCATAGGGCAGGCTTTATT	9034
Qy	1975	TTTTAAATGGTAATA--GATATCACTTGAGGTTTTTATCAAAGAGTTGGCGGGGTGGT	2031
Db	9035	TTTTAAATGGTAATAGATGATATCACTTGAGGTTTTTATCAAAGAGTTGGCGGGGTGGT	9094
Qy	2032	AAAGTTCAACAACAGATTGAGGTTTTGTTTGCCAGATCTCAATTTTACATGTTTCTTT	2091
Db	9095	AAAGTTCAACAACAGATTGAGGTTTTGTTTGCCAGATCTCAATTTTACATGTTTCTTT	9154
Qy	2092	TGCAAAAGGTGATTTTTTTAAATAACATTTGTTTTCTCTTATCTTGTTTTATTAGGTC	2151
Db	9155	TGCAAAAGGTGATTTTTTTAAATAACATTTGTTTTCTCTTATCTTGTTTTATTAGGTC	9214
Qy	2152	GGAGACATGAGAAAACAGCGTCAAAATCATCTTTTCATGATCCCAAGCTGAAGGCGAGCC	2211
Db	9215	GGAGACATGAGAAAACAGCGTCAAAATCATCTTTTCATGATCCCAAGCTGAAGGCGAGCC	9274
Qy	2212	CTCCAGAGCGTTATGTGACCCACAACCGAGCACATTGGTGACAGACCTTCGGGGCCTG	2271
Db	9275	CTCCAGAGCGTTATGTGACCCACAACCGAGCACATTGGTGACAGACCTTCGGGGCCTG	9334
Qy	2272	TCTGAAGCCATAGCCTCCACGGAGAGCCCT	2301
Db	9335	TCTGAAGCCATAGCCTCCACGGAGAGCCCT	9364

## RESULT 5

ABK83778  
ID ARK83778 standard: cDNA: 12461 BP.

AC ABK83778;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #349.

Human; ss: granulocytic cell; DNA chip; bacterial infection;  
viral infection; parasitic infection; protozoal infection;  
fungal infection; sterile inflammatory disease; psoriasis;  
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
cardiac reperfusion injury; renal reperfusion injury; ARDS;  
adult respiratory distress syndrome; inflammatory bowel disease;  
Crohn's disease; ulcerative colitis; periodontal disease;  
granulocyte activation; chronic inflammation; allergy.

xx Homo sapiens.

PN WO200228999-A2.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US030821.

PR 03-OCT-2000; 2000US-0237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 349; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 12461 BP; 3372 A; 2728 C; 2816 G; 3544 T; 0 U; 1 Other;

ry Match 97.4%; Score 2241.6; DB 6; Length 12461;

t Local Similarity	99.3%	Pred. No. 0;
	Score 2241.6	

ches 2294; Conservative 1; Mismatches 5; Indels 10;

Qy 1 CTGAAATGATGCTCCCAAGTGCTATGTGATGAGCTCCTTGTGTGCCCAGTGGAATAGGTG 60

Db 7056 CTGAAATGATGCTCCCAAGTGCTATGTGATGAGCTCCTTGTGTGCCAGTGCATAGGTG 7115

QV 61 TGTCCATGTGTCA TTTTAAAGACTATTAA TTACACTAATATAGTTTCTTCTCTCTTGG 120

db 7116 TGCCATGTGTCATTTTAAGACTATTAAATCACATAATAGTTTCTTCTCTTGG 7175

121 ATAATAGGACGTTGTTCCGTA TGGACTTGGAGGCCCTAGGTC CAAAGAGAGCCTTGGAGC 180

7176 ATAA TAGGACCGTTGTTCCGTATTCGACTTGGCAAGCCCTTCCCTCCAGACGACCTTCCGCA 7235

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Qy	301	TGCTTTTCAATCAGTTTAACAGAGCCICTGAACCTCCTTCCTATCATGGTACTGCCTTCCTG	360
Db	7356	TGCTTTTCAATCAGTTTAACAGAGCCTCCTGAACCTCCTTCCTATCATGGTACTGCCTTCCTG	7415
Qy	361	TTTTAGAGAGACTAAACAGAGACATTGAAGCTCAGGCTAAGCTGAATATAAACATTGCTGA	420
Db	7416	TTTTTAGAGAGACTAAACAGAGACATTGAAGCTCAGGCTAAGCTGAATATAAACATTGCTGA	7475
Qy	421	AATGTTTTTCTTGTTATTTTAAACAGGGCTGAAGACATTATCGAGAAGAGACTGGAAATAA	480
Db	7476	AATGTTTTTCTTGTTATTTTAAACAGGGCTGAAGACATTATCGAGAAGAGACTGGAAATAA	7535
Qy	481	TCATAAGAAAGGAAAAAGACTGTTTCCAAGCTTGGGAAAAAGTGTATTATTACGACAGTTAGT	540
Db	7536	TCATAAGAAAGGAAAAAGACTGTTTCCAAGCTTGGGAAAAAGTGTATTATTACGACAGTTAGT	7595
Qy	541	GAGAGNAGAAAATCAGAAGAAGTTTCAGNGBAACHCCTTAAGCAAACCAGGTAAAGGG	600
Db	7596	GAGAGNAGAAAATCAGAAGAAGTTTCAGAGGAACACCTTAAGCAAACCAGGTAAAGGG	7655
Qy	601	AAGGAAAGAAAAATTAGGTAAAGAGTTTACAAGAAACAATAGCCCCCAGTCAGTCATGCCAG	660
Db	7656	AAGGAAAGAAAAATTAGGTAAAGAGTTTACAAGAAACAATAGCCCCCAGTCAGTCATGCCAG	7715
Qy	661	CAGCCTGTTCTCCAGGCCCTTCTTACCCGGCAGGTGAAGACTTGAACACAGTAGCACG	720
Db	7716	CAGCCTGTTCTCCAGGCCCTTCTTACCCGGCAGGTGAAGACTTGAAGAAACAGTAGCACG	7775
Qy	721	AGGAGATCTATGCATCCTATAGATTAAAAAGGACAAAAGAAATCCCCTTTAAATATATTCCA	780
Db	7776	AGGAGATCTATGCATCCTATAGATTAAAAAGGACAAAAGAAATCCCCTTTAAATATATTCCA	7835
Qy	781	TGAGCTCTGGAAATGAAAACCGATGTCCTCTGTACTTTTAGACATACCATTTTCATCTAC	840
Db	7836	TGAAGCTCTGGAAATGAAAACCGATGTCCTCTGTACTTTTAGACATACCATTTTCATCTAC	7895
Qy	841	AGGTAGATTTCCCAACCAAAAATATATCCAGAGATGCCTTTGTCAATGGGTATATACAGC	900
Db	7896	AGGTAGATTTCCCAACCAAAAATATATCCAGAGATGCCTTTGTCAATGGGTATATACAGC	7955
Qy	901	CTTTTGCTCTGAGTCAATGTATTTACACATTTCCCTGAGAAATCGAAAATCATTTTGG	960
Db	7956	CTTTTGCTCTGAGTCAATGTATTTTACCACATTTCCCTGAGAAATCGAAAATCATTTTGG	8015
Qy	961	GGAGCGGACATTTAGAAAAAGAAATCAAAGTGTCAATGAATAATCTTCAATAAGTT	1020
Db	8016	GGAGCGGACATTTAGAAAAAGAAATCAAAGTGTCAATGAATAATCTTCAATAAGTT	8075
Qy	1021	GCAGTTATTTCAGATGCCCAAGGAAAAATTAAGTCATTAGATAGGGTTGGTAGAATTTAG	1080
Db	8076	GCAGTTATTTCAGATGCCCAAGGAAAAATTAAGTCATTAGATAGGGTTGGTAGAATTTAG	8135
Qy	1081	AACATGCTGTTTTCCAGGTTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG	1135
Db	8136	AACATGCTGTTTTCCAGGTTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG	8195
Qy	1136	AAATGTGTTTGGTGAGAGCCAAATGTCAATCCAAAGAGCTCTCTTTTCCCTGGTCAGTC	1195
Db	8196	AAATGTGTTTGGTGAGAGCCAAATGTCAATCCAAAGAGCTCTCTTTTCCCTGGTCAGTC	8255
Qy	1196	ATGTGCTGGGACAGAAAGGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGCTGC	1255
Db	8256	ATGTGCTGGGACAGAAAGGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGCTGC	8315
Qy	1256	TCTTTGGTGATAACCCCTTCCAATCCTAACTTTTGGAAATTCACAGCTCAAGAGGAGA	1315
Db	8316	TCTTTGGTGATAACCCCTTCCAATCCTAACTTTTGGAAATTCACAGCTCAAGAGGAGA	8375
Qy	1316	AACCTACTCTGATCTACCATGTTCTGCAATTTTCTATCATGGTCTATGAAACTTC	1375
Db	8376	AACCTACTCTGATCTACCATGTTCTGCAATTTTCTATCATGGTCTATGAAACTTC	8435

QY	1376	TCTTAGAAATCCAGTGGCAAGAGTTCTATGATTAAAGTGTCTGAGCTCAGGCCAGGCA	1435	DB	Human nucleic acid sequence.
Db	8436	TCTTAGAAATCCAGTGGCAAGAGTTCTATGATTAAAGTGTCTGAGCTCAGGCCAGGCA	8495	KW	Human; antisense; lung dysfunction; nasal airway dysfunction;
QY	1436	GTCATGAACACTCTCTGAGTATTTACTACTGATTTGTGGGCGCCTCAGCTATCGTT	1495	KW	antiinflammatory steroid; ubiquinone; antinflammatory; antiallergic;
Db	8496	GTCATGAACACTCTCTGAGTATTTACTACTGATTTGTGGGCGCCTCAGCTATCGTT	8555	KW	antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
QY	1496	TCTTACACACTCTCTATGAGATATCCCATATTTATGTCGCGAGGCCAGTAATGCTCCCA	1555	KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
Db	8556	TCTTACACACTCTCTATGAGATATCCCATATTTATGTCGCGAGG-CAGTAATGCTCCCA	8614	KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
QY	1556	CGAGATCAGTTCTGAACTAACCTGGAAATTTTATGAGGTTTATATGCAACTATTA	1615	OS	lung inflammation; respiratory disease; ds.
Db	8615	CGAGATCAGTTTCTGAACTAACCTGGAAATTTTATGAGGTTTATATGCAACTATTA	8674	XX	Homo sapiens.
QY	1616	AATCAACATTTACAGTTCTTCCCTCTGTTTCTCTGTAATAACATTAGGCTGCAAAAA	1675	XX	WO200285308-A2.
Db	8675	AATCAACATTTACAGTTCTTCCCTCTGTTTCTCTGTAATAACATTAGGCTGCAAAAA	8734	XX	31-OCT-2002.
QY	1676	AAAAAATCTTTTAAAAATAATGTCATAAGTATTTGCTCGGCCCTACTGTATGCTTC	1735	XX	23-APR-2002; 2002WO-US013135.
Db	8735	AAAAAATCTTTTAAAAATAATGTCATAAGTATTTGCTCGGCCCTACTGTATGCTTC	8794	XX	24-APR-2001; 2001US-0286137P.
QY	1736	TTTTCTTTTCTCTCTTTCAACTAAGTCACCGTCAATTTATTAAGATGGCCAACTAT	1795	XX	(EPIC-) EPIGENESIS PHARM INC.
Db	8795	TTTTCTTTTCTCTCTTTCAACTAAGTCACCGTCAATTTATTAAGATGGCCAACTAT	8854	XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
QY	1796	TCAAAACCTATGCTGAGTTTCTCAAGCGAGGCTCATAGTATGATGAAGTTGGATGGG	1855	PI	Miller S, Tang L, Shahabuddin S;
Db	8855	TCAAAACCTATGCTGAGTTTCTCAAGCGAGGCTCATAGTATGATGAAGTTGGATGGG	8914	XX	WPI; 2003-229219/22.
QY	1856	CTACGGAAGAACCGAACAACCTAGTTTATTTAAACCTGTATTTACTGCCACTTCC	1915	XX	Pharmaceutical composition for treating ailments associated with impaired
Db	8915	CTACGGAAGAACCGAACAACCTAGTTTATTTAAACCTGTATTTACTGCCACTTCC	8974	XX	respiration, has oligo(s) antisense to specific gene(s) or its
QY	1916	CCTTAGACTTGACCATATGACCCCTCGGT-CGCATTTAAGCATAGGCGCAGGCTTTATT	1974	XX	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
Db	8975	CCTTAGACTTGACCATATGACCCCTCGGT-CGCATTTAAGCATAGGCGCAGGCTTTATT	9034	XX	ubiquinone.
QY	1975	TTTACAATGGTAATA--GATATCACTTGAGGTTTATCAAGAGTTGCGGGGGTGGTG	2031	XX	Disclosure; SEQ ID NO 12225; 872pp; English.
Db	9035	TTTACAATGGTAATAGATGATATCACTTGAGGTTTATCAAGAGTTGCGGGGGTGGTG	9094	XX	The invention relates to a novel pharmaceutical composition, which has a
QY	2032	AAAGTTTCAACACAGATTTCAGGTTTGTGTGCGAGATTCTAAATTTACATGTTTCTTT	2091	XX	first active agent comprising an oligonucleotide antisense to the
Db	9095	AAAGTTTCAACACAGATTTCAGGTTTGTGTGCGAGATTCTAAATTTACATGTTTCTTT	9154	XX	initiation codon, coding region, 5' or 3' end genomic flanking regions,
QY	2092	TGCCAAAGGGTGATTTTTTAAATAACAATTTGTTTCTTATCTTATCTGTTTATAGTGC	2151	XX	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
Db	9155	TGCCAAAGGGTGATTTTTTAAATAACAATTTGTTTCTTATCTTATCTGTTTATAGTGC	9214	XX	junctions of genes encoding a polypeptide associated with lung and/or
QY	2152	GGAGACCATGAGAAACAGCGTCAATCATCTTTTCATGATCCCAAGCTGAAAGGCAAGCC	2211	XX	nasal airway dysfunction and a second active agent comprising an
Db	9215	GGAGACCATGAGAAACAGCGTCAATCATCTTTTCATGATCCCAAGCTGAAAGGCAAGCC	9274	XX	antiinflammatory steroid and ubiquinone. A composition of the invention
QY	2212	CTCCAGAGAGCGTTATGTGACCCCAACACCGAGCACATTTGGTGACAGACCTTCGGGGCCTG	2271	XX	has antiinflammatory, antiallergic, antiasthmatic, hypotensive, or
Db	9275	CTCCAGAGAGCGTTATGTGACCCCAACACCGAGCACATTTGGTGACAGACCTTCGGGGCCTG	9334	XX	immunosuppressive, and cytostatic activity. The composition may have a
QY	2272	TCTGAAGCCATAGCTCCACGAGAGCCCT	2301	XX	use in antisense gene therapy. The composition is useful for treating or
Db	9335	TCTGAAGCCATAGCTCCACGAGAGCCCT	9364	XX	preventing a respiratory, lung or malignant disease or condition, also
QY	2301	TCTGAAGCCATAGCTCCACGAGAGCCCT	2364	XX	for enhancing the prophylactic or therapeutic respiratory effect of an
Db	2364	TCTGAAGCCATAGCTCCACGAGAGCCCT	2420	XX	antiinflammatory steroid in a subject, for reducing or depleting levels
QY	2420	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2480	XX	of, or reducing sensitivity to adenosine, reducing levels of adenosine
Db	2480	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2540	XX	receptor, producing bronchodilation, increasing levels of ubiquinone or
QY	2540	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2600	XX	lung surfactant in a subject's tissue, or treating bronchoconstriction,
Db	2600	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2660	XX	lung inflammation, lung allergies, or a respiratory disease or condition.
QY	2660	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2720	XX	Note: The sequence data for this patent is not represented in the printed
Db	2720	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2780	XX	specification, but was obtained in electronic format directly from WIPO
QY	2780	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2840	XX	at ftp.wipo.int/pub/published_pct_sequences
Db	2840	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2900	XX	Sequence 12461 BP; 3372 A; 2728 C; 2816 G; 3544 T; 0 U; 1 Other;
QY	2900	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	2960	XX	Query Match 97.4%; Score 2241.6; DB 7; Length 12461;
Db	2960	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	3020	XX	Best Local Similarity 99.3%; Pred. No. 0;
QY	3020	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	3080	XX	Matches 2294; Conservative 1; Mismatches 5; Indels 10; Gaps 4;
Db	3080	ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG	3140	XX	QY 1 CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC 60
QY	3140	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3200	XX	Db 7056 CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC 7115
QY	3200	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3260	XX	QY 61 TGTCATGTGTCATTTTAAAGACTATTAACTACACTAATATAGTTTCTCTCTTTGG 120
Db	3260	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3320	XX	Db 7116 TGTCATGTGTCATTTTAAAGACTATTAACTACACTAATATAGTTTCTCTCTTTGG 7175
QY	3320	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3380	XX	QY 121 ATAATAGGACGTTGTTCCGATAGGACTTGGAGCCCTAGTCCAGAGAGCCCTTGAGA 180
Db	3380	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3440	XX	Db 7176 ATAATAGGACGTTGTTCCGATAGGACTTGGAGCCCTAGTCCAGAGAGCCCTTGAGA 7235
QY	3440	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3500	XX	QY 181 ATTTACTTCCCAAAAGGCCAACACCGTCAATAGATCCCAATAGTGTCTAGCCAAAAG 240
Db	3500	CTGAATGATGCTCCCAAGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTGC	3560	XX	

RESULT 6  
ABZ96983  
ID ABZ96983 standard; DNA; 12461 BP.  
XX  
AC ABZ96983;  
XX  
DT 17-OCT-2003 (first entry)  
XX

Db 7236 ATTTACTTCCCAAGGCAACAGACCGGTGAGATAGATGCAATGTGCTAGCCAAAAG 7295  
QY 241 ACAAGAAGTCTGGAAATTTTCCCAAGCAGAGAAAGAACTCAGGTGACAGAAACACCTT 300  
Db 7296 ACAAGAAGTCTGGAAATTTTCCCAAGCAGAGAAAGAACTCAGGTGACAGAAACACCTT 7355  
QY 301 TCGTTTTCATCAGTTTAAACAGCCCTCCTGAACTCCTTCTCTATCATGTTACTGCTTCTG 360  
Db 7356 TCGTTTTCATCAGTTTAAACAGCCCTCCTGAACTCCTTCTCTATCATGTTACTGCTTCTG 7415  
QY 361 TTTTATAGAGACTAAACAGAGACATTGAAAGTCAGGTGAAAGCTGAATATTAACATTGCTGA 420  
Db 7416 TTTTATAGAGACTAAACAGAGACATTGAAAGTCAGGTGAAAGCTGAATATTAACATTGCTGA 7475  
QY 421 AATGTTTTTCTTGTGTATTTTAAACAGGCTGAAGACATTTATGAGAAAGACTGGAATAA 480  
Db 7476 AATGTTTTTCTTGTGTATTTTAAACAGGCTGAAGACATTTATGAGAAAGACTGGAATAA 7535  
QY 481 TCATAGAGAAAGAAAGACTGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAG 540  
Db 7536 TCATAGAGAAAGAAAGACTGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAG 7595  
QY 541 GAGAGAAAGAAATCAGAAAGTTCAGAGGAAACACCTTAAGACAAACAGGTAAAGAGG 600  
Db 7596 GAGAGAAAGAAATCAGAAAGTTCAGAGGAAACACCTTAAGACAAACAGGTAAAGAGG 7655  
QY 601 AAGGAGAAATTAAGTAAAGGTTTCAAGAGCAACTAGCCCGAGTCAGTATGTCAG 660  
Db 7656 AAGGAGAAATTAAGTAAAGGTTTCAAGAGCAACTAGCCCGAGTCAGTATGTCAG 7715  
QY 661 CAGCTGTCTCTCCAGCCCTTCTTACCCGCGGAGGTGAAAGTTCAGAGTTCAGAGTTCAG 720  
Db 7716 CAGCTGTCTCTCCAGCCCTTCTTACCCGCGGAGGTGAAAGTTCAGAGTTCAGAGTTCAG 7775  
QY 721 AGGAGATCTATGATCTTATAGATTAAAGAGGAGAAAGAAATCCCTCTTAAATATTTCCA 780  
Db 7776 AGGAGATCTATGATCTTATAGATTAAAGAGGAGAAAGAAATCCCTCTTAAATATTTCCA 7835  
QY 781 TGAAGCTCTGGAATCAGAAACGATGCTCTGTACTTTTACACATACCATTTTCACTAC 840  
Db 7836 TGAAGCTCTGGAATCAGAAACGATGCTCTGTACTTTTACACATACCATTTTCACTAC 7895  
QY 841 AGGTAGATTTCCAAACCAAAATATATCCAGAGTGCCTTTCTCATGGGTTATATACAGC 900  
Db 7896 AGGTAGATTTCCAAACCAAAATATATCCAGAGTGCCTTTCTCATGGGTTATATACAGC 7955  
QY 901 CTTTGCCTCTCTGAGTCAATGATTTTACCACTTTTCCCTGAGAAATCGAAATCATTTTGG 960  
Db 7956 CTTTGCCTCTCTGAGTCAATGATTTTACCACTTTTCCCTGAGAAATCGAAATCATTTTGG 8015  
QY 961 GGAGCGGACATTTAGAAAAAGAAATCAAAAGTCTCATGGAATCAAAATCTTCAATAAGTT 1020  
Db 8016 GGAGCGGACATTTAGAAAAAGAAATCAAAAGTCTCATGGAATCAAAATCTTCAATAAGTT 8075  
QY 1021 CGAGTTATTCAGATGCGCAAGGAAATTAAGTCAATAGATAGGTTGGTAGAATTTAG 1080  
Db 8076 CGAGTTATTCAGATGCGCAAGGAAATTAAGTCAATAGATAGGTTGGTAGAATTTAG 8135  
QY 1081 AACATGCTGTTTTTTCAGGTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 1135  
Db 8136 AACATGCTGTTTTTTCAGGTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 8195  
QY 1136 AAATGTTTTGTTGTCAGAGCAATGTCATTCGAAAGCTCTCTCTTTTCTGTCAGTC 1195  
Db 8196 AAATGTTTTGTTGTCAGAGCAATGTCATTCGAAAGCTCTCTCTTTTCTGTCAGTC 8255  
QY 1196 ATGTCCTGGGACAGAGAGGATCTGGATTAGGCAACATCATAGATTTGCTCTGAGCTGC 1255  
Db 8256 ATGTCCTGGGACAGAGAGGATCTGGATTAGGCAACATCATAGATTTGCTCTGAGCTGC 8315  
QY 1256 TCTTTGGTGAATACCTTCCAAATCTTAACTTTTGGAAATTCAGAGTCAAGAGGAGGA 1315

Db 8316 TCTTTGGTGAATACCTTCCAAATCTTAAACTTTTGGAAATTCAGAGTCAAGAGGAGGA 8375  
QY 1316 AACCTACTCTCTGATCTACACATGTTCTGCAATTTTCTTATCATGTTCTATGAAACTTC 1375  
Db 8376 AACCTACTCTCTGATCTACACATGTTCTGCAATTTTCTTATCATGTTCTATGAAACTTC 8435  
QY 1376 TCTTAGAATCCAGTGGGCAAGGTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 1435  
Db 8436 TCTTAGAATCCAGTGGGCAAGGTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 8495  
QY 1436 GTCATGAACTACTCTCTGAGTTATTTACTACTGATTTTGGGCGAGCTCAGCTATCGGTT 1495  
Db 8496 GTCATGAACTACTCTCTGAGTTATTTACTACTGATTTTGGGCGAGCTCAGCTATCGGTT 8555  
QY 1496 TCTTCAACCTGCTTATGAGAGTATCCATATTTATGTTGTCGAGGCCAGTATGCTCCCA 1555  
Db 8556 TCTTCAACCTGCTTATGAGAGTATCCATATTTATGTTGTCGAGGCCAGTATGCTCCCA 8614  
QY 1556 CGAGATCAGTTCTGAACTAACTGGAATTTTATGTTGTTTATGTTGTTTATGTTGTTTAT 1615  
Db 8615 CGAGATCAGTTCTGAACTAACTGGAATTTTATGTTGTTTATGTTGTTTATGTTGTTTAT 8674  
QY 1616 AATCAACATTACAGTTCTTCTCTGATTTCTCTGTAATTTCTCTGTAATAAATAGGCTGCAAAAA 1675  
Db 8675 AATCAACATTACAGTTCTTCTCTGATTTCTCTGTAATTTCTCTGTAATAAATAGGCTGCAAAAA 8734  
QY 1676 AAAAAATCTTTTAAATAATGTCATTAAGTATTTGCTCTGCGGCTACTGATGCTTC 1735  
Db 8735 AAAAAATCTTTTAAATAATGTCATTAAGTATTTGCTCTGCGGCTACTGATGCTTC 8794  
QY 1736 TTTTCTTTTCTCTCTTTTCAACTAAGTCACCGTCAATTTATTAAGATGCGCATTAAT 1795  
Db 8795 TTTTCTTTTCTCTCTTTTCAACTAAGTCACCGTCAATTTATTAAGATGCGCATTAAT 8854  
QY 1796 TCAAAACCTATGCTGATGTTCTCAAGGCGAGGTTCATAGTATGATGAAAGTGGGATGGG 1855  
Db 8855 TCAAAACCTATGCTGATGTTCTCAAGGCGAGGTTCATAGTATGATGAAAGTGGGATGGG 8914  
QY 1856 CTACGGAAGAAACCAAGAACAACTAGTTTATTTAAACCTGTATTTACTGCCACTTCC 1915  
Db 8915 CTACGGAAGAAACCAAGAACAACTAGTTTATTTAAACCTGTATTTACTGCCACTTCC 8974  
QY 1916 CTTTAGACTTGACATATGACCCCTCGCT-CCATTTCTAAGCATAGGCGAGCTTTAT 1974  
Db 8975 CTTTAGACTTGACATATGACCCCTTGCTCCCATTTCTAAGCATAGGCGAGCTTTAT 9034  
QY 1975 TTTACAACTGGTAATA--GATATCACTTGAGGTTTTATCAAGAGTTGCGCGGCTGGT 2031  
Db 9035 TTTACAACTGGTAATAAGATGATATCACTTGAGGTTTTATCAAGAGTTGCGCGGCTGGT 9094  
QY 2032 AAAGTTCAACAAGATTCAGGTTTGTGTCAGATTTCAATTTTACATGTTTCTTT 2091  
Db 9095 AAAGTTCAACAAGATTCAGGTTTGTGTCAGATTTCAATTTTACATGTTTCTTT 9154  
QY 2092 TCCCAAGGCTGATTTTTTAAATAACATTTGTTTCTTCTTATCTTATCTTATGATGTC 2151  
Db 9155 TCCCAAGGCTGATTTTTTAAATAACATTTGTTTCTTCTTATCTTATCTTATGATGTC 9214  
QY 2152 GGAGACCATGAGAAACAGCGTCAAAATCATCTTTTATGATCCCAAGCTGAAAGCAAGCC 2211  
Db 9215 GGAGACCATGAGAAACAGCGTCAAAATCATCTTTTATGATCCCAAGCTGAAAGCAAGCC 9274  
QY 2212 CTTCCAGAGGCTTATGAGCCCAACCGAGCACTTGGTGAAGAGCTTGGGCGCTG 2271  
Db 9275 CTTCCAGAGGCTTATGAGCCCAACCGAGCACTTGGTGAAGAGCTTGGGCGCTG 9334  
QY 2272 TCTGAAGCCATAGCCTCCACGAGAGCCCT 2301  
Db 9335 TCTGAAGCCATAGCCTCCACGAGAGCCCT 9364

ID	ACA64929	standard; DNA; 12461 BP.
XX	ACA64929;	
AC		
XX		
DT	27-JUN-2003	(first entry)
XX		
XX	Human EDN1	DNA corresponding to J05008.
DE		
XX	Human;	chronic inflammatory joint disease; infection; tumour;
KW	antiflamatory;	cytostatic; antirheumatic; antineumatic;
KW	immunosuppressive;	gene therapy; etiological pathogenicity; ds.
XX		
OS	Homo sapiens.	
XX		
XX	DE10127572-A1.	
PN		
XX	05-DEC-2002.	
PD		
XX	30-MAY-2001;	2001DE-01027572.
PF		
XX	30-MAY-2001;	2001DE-01027572.
PR		
XX	(PATH-) PATHARRAY	GMBH.
PA		
XX	Haeupl T, Ungethuen U, Blaess S;	
PI		
XX	WPI; 2003-240797/24.	
DR		
XX	Reagents for diagnosis, study and therapy of chronic inflammatory joint	
PT	and other diseases, comprises any of many specified genes or derived	
PT	proteins.	
XX		
PS	Claim 1; Page; 12pp; German.	
XX		
CC	This invention describes a novel reagent for diagnosis, molecular	
CC	definition and therapy of chronic inflammatory joint diseases, and other	
CC	inflammatory disorders, infective or tumour diseases in humans. The	
CC	products of the invention have antiinflammatory, cytostatic,	
CC	antiarthritic, antirheumatic and immunosuppressive activity and can be	
CC	used for gene therapy. The reagent of the invention and any proteins and	
CC	antibodies derived from it, are used (i) for analysing tissue and blood	
CC	samples for medical diagnosis; (ii) for diagnosis and characterisation of	
CC	chronic joint diseases, on the basis of molecular characterisation, and	
CC	determining the etiological pathogenicity principle of as yet	
CC	uncharacterised inflammatory diseases, also monitoring progression and/or	
CC	treatment of disease, and optimisation of therapy and (iii) for	
CC	developing treatments for inflammatory diseases, particularly of joints,	
CC	infections and tumours. ACA64801-ACA64965 represent human polynucleotides	
CC	used in the method of the invention	
XX		
SQ	Sequence 12461 BP; 3372 A; 2728 C; 2816 G; 3544 T; 0 U; 1 Other;	
	Query Match 97.4%; Score 2241.6; DB 7; Length 12461;	
	Best Local Similarity 99.3%; Pred. NC. 0;	
	Matches 2294; Conservative 1; Mismatches 5; Indels 10; Gaps 4;	
QY	1	CTGAATGATGCTCCCAAGCTGTAATGATGAGCTCCTGTGTGCGCCAGTGGAAATAGTG 60
DB	7056	CTGAATGATGCTCCCAAGCTGTAATGATGAGCTCCTGTGTGCGCCAGTGGAAATAGTG 7115
QY	61	TGTCCATGTGCTATTTAAAGACTATTAATACACTAATATAGTTCTCTCTCTTGG 120
DB	7116	TGTCCATGTGCTATTTAAAGACTATTAATACACTAATATAGTTCTCTCTCTTGG 7175
QY	121	ATAATAGGACCTGTTCCGATGAGCTTGGAGCCCTAGTCCAGAGAGCCCTGGAGA 180
DB	7176	ATAATAGGACCTGTTCCGATGAGCTTGGAGCCCTAGTCCAGAGAGCCCTGGAGA 7235
QY	181	ATTACTTCCCAAGGCAACAGACCGTGAATAATAGATGCCAATGCTAGCCAAAG 240
DB	7236	ATTACTTCCCAAGGCAACAGACCGTGAATAATAGATGCCAATGCTAGCCAAAG 7295
QY	241	ACAAGAAGTGTGGAAATTTTCCCAAGGCAACAGACCGTGAATAATAGATGCCAATGCTAGCCAAAG 300

Db 8376 AACCTACTCTGTGATCTACCAATGTTCTGCAATTTTCTATCATGGTCTATGGAATTC 8435  
QY 1376 TCTTGAATCAGTGGCAAGAGTTCTATGATTAAGTGTCTGAGCTCAGGCAGGCA 1435  
Db 8436 TCTTGAATCAGTGGCAAGAGTTCTATGATTAAGTGTCTGAGCTCAGGCAGGCA 8495  
QY 1436 GTCATGAATCTCTGAGTGTATTTACTACTGATTTGCGGCGCAGCTCAGCTATCGGT 1495  
Db 8496 GTCATGAATCTCTGAGTGTATTTACTACTGATTTGCGGCGCAGCTCAGCTATCGGT 8555  
QY 1496 TCTTCAACCTGCTTATGAGAGTATCCATATTTATGTCGAGGCGAGTAATGCTCCCA 1555  
Db 8556 TCTTCAACCTGCTTATGAGAGTATCCATATTTATGTCGAGGCGAGTAATGCTCCCA 8614  
QY 1556 CGAGATCAGTTCTGAACTAACCTGGAATTTTATGCGGTTTATATGCACTATTA 1615  
Db 8615 CGAGATCAGTTCTGAACTAACCTGGAATTTTATGCGGTTTATATGCACTATTA 8674  
QY 1616 AATCAACATTCAGTCTTCCCTCTGATTTCTCTGTAAACATTTAGGCTCGCAAAA 1675  
Db 8675 AATCAACATTCAGTCTTCCCTCTGATTTCTCTGTAAACATTTAGGCTCGCAAAA 8734  
QY 1676 AAAAAATCTTTAAAAATAATGTCATAAATTTCTCTGGGCTTCTGATGCTTC 1735  
Db 8735 AAAAAATCTTTAAAAATAATGTCATAAATTTCTCTGGGCTTCTGATGCTTC 8794  
QY 1736 TTTTCTTTTCTCTCTTTTCACTAAGTCACGCTCAATTTTATTAAGTGGCCATAACTAT 1795  
Db 8795 TTTTCTTTTCTCTCTTTTCACTAAGTCACGCTCAATTTTATTAAGTGGCCATAACTAT 8854  
QY 1796 TCAAAACCTATGCTGAGTTCCTCAAGCAGGCTCAGATGATGATCAAGTTGGATGGG 1855  
Db 8855 TCAAAACCTATGCTGAGTTCCTCAAGCAGGCTCAGATGATGATCAAGTTGGATGGG 8914  
QY 1856 CTACGGAGAACACGACCACTCTAGTTTATTAACCTGATTTTACTGCCACTTCC 1915  
Db 8915 CTACGGAGAACACGACCACTCTAGTTTATTAACCTGATTTTACTGCCACTTCC 8974  
QY 1916 CTTAGACTTGACCATATGACCCCTCGCT-CCCATTTCTAAGCAGGAGGCTTTATT 1974  
Db 8975 CTTAGACTTGACCATATGACCCCTCGCT-CCCATTTCTAAGCAGGAGGCTTTATT 9034  
QY 1975 TTTCAATGGTAATA--GATATCATCTGAGTTTATCAAGAGTTGCGCGGGTGGT 2031  
Db 9035 TTTCAATGGTAATAAGATGATATCATCTGAGTTTATCAAGAGTTGCGCGGGTGGT 9094  
QY 2032 AAAAGTTCAACACGATTCAGGTTTGTGTCGAGATTTCTAATTTTACATGTTTCTTT 2091  
Db 9095 AAAAGTTCAACACGATTCAGGTTTGTGTCGAGATTTCTAATTTTACATGTTTCTTT 9154  
QY 2092 TCCAAAGGAGTATTTTAAATAACATTTGTTTGTGTCGAGATTTCTAATTTTACATGTTTCTTT 2151  
Db 9155 TGCCAAAGGAGTATTTTAAATAACATTTGTTTGTGTCGAGATTTCTAATTTTACATGTTTCTTT 9214  
QY 2152 GGAGACCATGAGAACAGCTCAATATCTTTTATGATCCCAAGCTGAAAGGCAAGCC 2211  
Db 9215 GGAGACCATGAGAACAGCTCAATATCTTTTATGATCCCAAGCTGAAAGGCAAGCC 9274  
QY 2212 TTCCAGAGAGGTTATGATGACCCCAACCCAGAGCAATTTGTTGACAGACCTTTGCGGGCTG 2271  
Db 9275 TTCCAGAGAGGTTATGATGACCCCAACCCAGAGCAATTTGTTGACAGACCTTTGCGGGCTG 9334  
QY 2272 TCTGAGCCATAGCTCTCCACGAGAGCCCT 2301.  
Db 9335 TCTGAGCCATAGCTCTCCACGAGAGCCCT 9364

## RESULT 8

AAA35170 standard; DNA; 14879 BP.

XX AAA35170;

AC AAA35170;

XX

DT 28-JUL-2000 (first entry)  
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:44.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiasthmatic; cytotstatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX Homo sapiens.  
OS  
XX WO200009525-A2.  
FN  
XX  
PD 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
PF  
XX  
XX 03-AUG-1998; 98US-0095212P.  
PR  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
PA  
XX  
XX Nyce JW;  
PI  
XX  
XX WPI; 2000-205971/18.  
DR  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 1201-1205; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3213 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 14879 BP; 3971 A; 3370 C; 3434 G; 4103 T; 0 U; 1 Other;

Query Match 97.4%; Score 2241.6; DB 3; Length 14879;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 2294; Conservative 1; Mismatches 5; Indels 10; Gaps 4;

QY 1 CTGAATGATGCTCCCAAGTGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTG 60

Db 7056 CTGAATGATGCTCCCAAGTGTCTATGATGAGCTCTCTGTGTCGCCAGTGAATAGTG 7115

QY 61 TGTCACATGTCATTTTAAAGACTATTATACATAATAGTTCTTCTCTCTTGG 120

Db 7116 TGTCCATGTGTCATTTTAAAGACTATTAATACACTAATATAGTTCTCTCTCTTGG 7175  
QY 121 ATAATAGGACGTTGTTGCGTATGACCTTGAAGCCCTAGTTCGAAGAGCCCTTGGAGA 180  
Db 7176 ATAATAGGACGTTGTTGCGTATGACCTTGAAGCCCTAGTTCGAAGAGCCCTTGGAGA 7235  
QY 181 ATTTACTTCCCAAAAGGCAACAGACCGTGAAGATAGATGCAATGTCTAGCCAAAG 240  
Db 7236 ATTTACTTCCCAAAAGGCAACAGACCGTGAAGATAGATGCAATGTCTAGCCAAAG 7295  
QY 241 ACAAGAGTGTGGAAATTTTCCAAAGCAGGAAGAACTCAGGTGAGCAAAACACCTT 300  
Db 7296 ACAAGAGTGTGGAAATTTTCCAAAGCAGGAAGAACTCAGGTGAGCAAAACACCTT 7355  
QY 301 TGTCTTTCAATCAGTTTAAAGCCCTCTGAACCTCTCTCATCTGTTGCTTCTCTG 360  
Db 7356 TGTCTTTCAATCAGTTTAAAGCCCTCTGAACCTCTCTCATCTGTTGCTTCTCTG 7415  
QY 361 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGGTAAAGCTGAATAACATTGCTGA 420  
Db 7416 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGGTAAAGCTGAATAACATTGCTGA 7475  
QY 421 AATGTTTTCTTGTGTTATTTAAAGGCTGAAGACATTTAGGAGAAAGACTGGAATAA 480  
Db 7476 AATGTTTTCTTGTGTTATTTAAAGGCTGAAGACATTTAGGAGAAAGACTGGAATAA 7535  
QY 481 TCATAAGAAAGAAAGACTGTTCCAAAGCTTGGGAAAGTGTATTTATCAGCAGTTAGT 540  
Db 7536 TCATAAGAAAGAAAGACTGTTCCAAAGCTTGGGAAAGTGTATTTATCAGCAGTTAGT 7595  
QY 541 GAGAGAGAAAGAAATCAGAGAAAGTTTCAAGAGAACACCTTAAGAACACAGGTAAGAGG 600  
Db 7596 GAGAGAGAAAGAAATCAGAGAAAGTTTCAAGAGAACACCTTAAGAACACAGGTAAGAGG 7655  
QY 601 AAGGAGAAAGAAATAGGTAAGAGTTTCAAGAGAACACCTAGCCAGTCAGTGTGCGAG 660  
Db 7656 AAGGAGAAAGAAATAGGTAAGAGTTTCAAGAGAACACCTAGCCAGTCAGTGTGCGAG 7715  
QY 661 CAGCCTGTTCTCCAGCCCTTCTTACCAGGAGGTTGAAAGACTTAGAAAAACAGTAGCAG 720  
Db 7716 CAGCCTGTTCTCCAGCCCTTCTTACCAGGAGGTTGAAAGACTTAGAAAAACAGTAGCAG 7775  
QY 721 AGGAGATCTATGATCCTATAGATTAAGAGGCAAGAAAGTCCCTCTTAATATTTCCA 780  
Db 7776 AGGAGATCTATGATCCTATAGATTAAGAGGCAAGAAAGTCCCTCTTAATATTTCCA 7835  
QY 781 TGAAGCTCTGGAATGCAAAACCGATGCTCTGTACTTTAGCACATACCATTTTCACTAC 840  
Db 7836 TGAAGCTCTGGAATGCAAAACCGATGCTCTGTACTTTAGCACATACCATTTTCACTAC 7895  
QY 841 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCTTGTGATGCTGTTATATACAGC 900  
Db 7896 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCTTGTGATGCTGTTATATACAGC 7955  
QY 901 CTCTTCCCTCTGAGTCAATGATTTTACACCTTCCCTGAGAAATCGAAATCATTTTGG 960  
Db 7956 CTCTTCCCTCTGAGTCAATGATTTTACACCTTCCCTGAGAAATCGAAATCATTTTGG 8015  
QY 961 GGAGCGGACATTTAGAAAGAAATCAAGTGTGATGATAATCAAAATCTTCAATAAGTT 1020  
Db 8016 GGAGCGGACATTTAGAAAGAAATCAAGTGTGATGATAATCAAAATCTTCAATAAGTT 8075  
QY 1021 CGAGTTATTCAGATGCGCAAGGAAATAAAGTCAATAGATAGGTTGGTGGATTTAG 1080  
Db 8076 CGAGTTATTCAGATGCGCAAGGAAATAAAGTCAATAGATAGGTTGGTGGATTTAG 8135  
QY 1081 AACATGCTGTTTTTTCAGGTTTATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135  
Db 8136 AACATGCTGTTTTTTCAGGTTTATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8195  
QY 1136 AACATGCTGTTTTTTCAGGTTTATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1195

Db 8196 AAATGTTGTTGGTGACAGCAATGTCATTTCAAAAAAGCTCTCTCTCTCTCTCTCTCT 8255  
QY 1196 ATGTGCTGGGACAGAGAGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGCTGC 1255  
Db 8256 ATGTGCTGGGACAGAGAGGATCTGGATTAGGCAACATCATAGAGTTGCTCTGAGCTGC 8315  
QY 1256 TCTTTGGTGATTAACCCCTTCCAAATCTTAACTTTTGGAAATTCACAAGCTCAAGAGGGA 1315  
Db 8316 TCTTTGGTGATTAACCCCTTCCAAATCTTAACTTTTGGAAATTCACAAGCTCAAGAGGGA 8375  
QY 1316 AACCTACTCTCTGATCTACACATGTTCTGCAATTTTCTATCATGCTCTATGGAACCTTC 1375  
Db 8376 AACCTACTCTCTGATCTACACATGTTCTGCAATTTTCTATCATGCTCTATGGAACCTTC 8435  
QY 1376 TCTTAGAATTCACAGTGCAGAGAGTCTATGATTTAAAGTGTCTGAGCTCAGGCCAGGCA 1435  
Db 8436 TCTTAGAATTCACAGTGCAGAGAGTCTATGATTTAAAGTGTCTGAGCTCAGGCCAGGCA 8495  
QY 1436 GTCATGAACCTCTCTGAGTTTACTACTGATTTGTGGGCGAGCTCAGCTATCGGTT 1495  
Db 8496 GTCATGAACCTCTCTGAGTTTACTACTGATTTGTGGGCGAGCTCAGCTATCGGTT 8555  
QY 1496 TCTTCCACACCTGTTATGAGAGTATCCATATTTATGTTGCGAGCCAGTAATGCTCCCCA 1555  
Db 8556 TCTTCCACACCTGTTATGAGAGTATCCATATTTATGTTGCGAGG-CAGTAATGCTCCCCA 8614  
QY 1556 CGAGATCAGTTTCTGAACTAACTGAAATTTTATGGGTTTTTATATGCCAACTATTA 1615  
Db 8615 CGAGATCAGTTTCTGAACTAACTGAAATTTTATGGGTTTTTATATGCCAACTATTA 8674  
QY 1616 AATCAACATTTAGAGTTCTTCCCTCTGATTTCTCTGTTAAACATTTAGGCTGCAAAAA 1675  
Db 8675 AATCAACATTTAGAGTTCTTCCCTCTGATTTCTCTGTTAAACATTTAGGCTGCAAAAA 8734  
QY 1676 AAAAAATCTTTTAAAAATAATTTGCCATAAAGTATTTGCTGGGCTTACTGTATGCTTC 1735  
Db 8735 AAAAAATCTTTTAAAAATAATTTGCCATAAAGTATTTGCTGGGCTTACTGTATGCTTC 8794  
QY 1736 TTTTCTTTTCTCTCTTTTCAACTAAGTCAACGCTCAATTTTAAAGTGGCCATAACTAT 1795  
Db 8795 TTTTCTTTTCTCTCTTTTCAACTAAGTCAACGCTCAATTTTAAAGTGGCCATAACTAT 8854  
QY 1796 TCAAAACCTATGCTGATTTCTCAAGCAGGCTCACAATAGTATGATGAGTTGGGATGGG 1855  
Db 8855 TCAAAACCTATGCTGATTTCTCAAGCAGGCTCACAATAGTATGATGAGTTGGGATGGG 8914  
QY 1856 CTACGGAAGAAACAGAACAACTCTAGTTTATTTAAACCTGTATTTACTGCCACTTCC 1915  
Db 8915 CTACGGAAGAAACAGAACAACTCTAGTTTATTTAAACCTGTATTTACTGCCACTTCC 8974  
QY 1916 CCTTAGACTTGACCATATGACCCCTCGCT-CCCATTTCAAGCATAGGGGAGGCTTTAT 1974  
Db 8975 CCTTAGACTTGACCATATGACCCCTCGCTCCCATTTCAAGCATAGGGGAGGCTTTAT 9034  
QY 1975 TTTTACATGTTAATA--GATATCACTTCAGGTTTATCAAAAGTGGGCGGGTGGTG 2031  
Db 9035 TTTTACATGTTAATAAGATGATATCACTTCAGGTTTATCAAGAGTTGGGCGGGTGGTG 9094  
QY 2032 AAAGTTCAACACAGATTCAGGTTTGTGTCAGATTTCTAAATTTTACATGTTCTTT 2091  
Db 9095 AAAGTTCAACACAGATTCAGGTTTGTGTCAGATTTCTAAATTTTACATGTTCTTT 9154  
QY 2092 TGCCTAAAGGTTGATTTTTTAAATAAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2151  
Db 9155 TGCCTAAAGGTTGATTTTTTAAATAAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9214  
QY 2152 GGAGACCATGAGAAACAGGCTCAAAATCATCTTTTCTATGATGCCAAGCTGAAAGCAAGCC 2211  
Db 9215 GGAGACCATGAGAAACAGGCTCAAAATCATCTTTTCTATGATGCCAAGCTGAAAGCAAGCC 9274  
QY 2212 CTCCAGAGAGCTTATGTCACCAACCGAGCACAATTTGTCAGACACTTGGGGCTG 2271  
Db 9275 CTCCAGAGAGCTTATGTCACCAACCGAGCACAATTTGTCAGACACTTGGGGCTG 9334

QY 2272 TCTGAAGCCATAGCTCCACGAGAGCCCT 2301  
 Db 9335 TCTGAAGCCATAGCTCCACGAGAGCCCT 9364

RESULT 9

AAF21292  
 ID AAF21292 standard; DNA; 14879 BP.

XX AAF21292;  
 XX AAF21292;

DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2859.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

XX WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

PS Disclosure; Page 1284-1288; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome

CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), CC pulmonary transplantation rejection, pulmonary infections, bronchitis, CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide CC fragments and antisense oligonucleotides used in the exemplification of CC the present invention

XX Sequence 14879 BP; 3971 A; 3370 C; 3434 G; 4103 T; 0 U; 1 Other;  
 SQ Query Match 97.4%; Score 2241.6; DB 3; Length 14879;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 2294; Conservative 1; Mismatches 5; Indels 10; Gaps 4;

QY 1 CTGAATGATGCTCCCAAGTGTATGTATGATGAGCTCTTGTGTCGCCAGTGAATAGTG 60  
 Db 7056 CTGAATGATGCTCCCAAGTGTATGTATGATGAGCTCTTGTGTCGCCAGTGAATAGTG 7115  
 QY 61 TGTCCATGTCATTTTAAAGACTATTATACACTAATATATAGTTTCTTCTCTTTGG 120  
 Db 7116 TGTCCATGTCATTTTAAAGACTATTATATACACTAATATAGTTTCTTCTCTTTGG 7175  
 QY 121 ATAATAGCAGCTTCTTCGTATGACTTGGAGCCCTAGTCCCAAGAGAGCCCTGGAGA 180  
 Db 7176 ATAATAGCAGCTTCTTCGTATGACTTGGAGCCCTAGTCCCAAGAGAGCCCTGGAGA 7235  
 QY 181 ATTTACTTCCCAAGGCAACAGACCCGTGAAATAGATGCAATGTCTAGCCAAAAG 240  
 Db 7236 ATTTACTTCCCAAGGCAACAGACCCGTGAAATAGATGCAATGTCTAGCCAAAAG 7295  
 QY 241 ACAAGAAGTCTGGAAATTTTTCGAAGCAGGAAAGAACTCAGGTGACGACAAACACCTT 300  
 Db 7296 ACAAGAAGTCTGGAAATTTTTCGAAGCAGGAAAGAACTCAGGTGACGACAAACACCTT 7355  
 QY 301 TGCCTTTCAATCAGTTTAAACAGCCCTCCTGAACTCCTTCTCTATCATGTGTACTGCTCTG 360  
 Db 7356 TGCCTTTCAATCAGTTTAAACAGCCCTCCTGAACTCCTTCTCTATCATGTGTACTGCTCTG 7415  
 QY 361 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGTAAGCTGAATATATACATGCTGA 420  
 Db 7416 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGTAAGCTGAATATATACATGCTGA 7475  
 QY 421 AATGTTTTCTTGTGTATTTTAAACAGGCTGAAACACATTTAGGAAAGAACTGGAATAA 480  
 Db 7476 AATGTTTTCTTGTGTATTTTAAACAGGCTGAAACACATTTAGGAAAGAACTGGAATAA 7535  
 QY 481 TCATAGAAAGGAAAGAGACTGTTCAGAGCTTTGGGAAAAAGTGTATTTATCAGAGTTAGT 540  
 Db 7536 TCATAGAAAGGAAAGAGACTGTTCAGAGCTTTGGGAAAAAGTGTATTTATCAGAGTTAGT 7595  
 QY 541 GAGAGGAGAGAAATCAGAGAGAGTTTCAGAGGACACCTTAAGACAAACAGGTAAGAGGG 600  
 Db 7596 GAGAGGAGAGAAATCAGAGAGAGTTTCAGAGGACACCTTAAGACAAACAGGTAAGAGGG 7655  
 QY 601 AAGGAGAGAGAAATAGGTAAGAGGTTCAAGAGCACTAGCCCGAGTCAGTGTAGCCAG 660  
 Db 7656 AAGGAGAGAGAAATAGGTAAGAGGTTCAAGAGCACTAGCCCGAGTCAGTGTAGCCAG 7715  
 QY 661 CAGCCTGTCTCCAGCCCTTCTTACCGGCGAGGTGAAGACTTTAGAAACAGTACAGCAG 720  
 Db 7716 CAGCCTGTCTCCAGCCCTTCTTACCGGCGAGGTGAAGACTTTAGAAACAGTACAGCAG 7775  
 QY 721 AGGAGATCTATCATCTTATAGATTAAGAGGAGCAAAAGAAATCCCTCTTAAATATTTCCA 780  
 Db 7776 AGGAGATCTATCATCTTATAGATTAAGAGGAGCAAAAGAAATCCCTCTTAAATATTTCCA 7835  
 QY 781 TGAAGCTCTGGAATGCAACCGATGCTCTGTACTTTTAGACATACCATTTCACTAC 840  
 Db 7836 TGAAGCTCTGGAATGCAACCGATGCTCTGTACTTTTAGACATACCATTTCACTAC 7895  
 QY 841 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCATTGGTTATATACAGC 900  
 Db 7896 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCATTGGTTATATACAGC 7955

QY 901 CTTTGGCTCTCTGAGTCAATGATTTACCACTTTCCCTGAGAAATCGAAATCATTTTGG 960  
DB 7956 CTTTGGCTCTCTGAGTCAATGATTTACCACTTTCCCTGAGAAATCGAAATCATTTTGG 8015  
QY 961 GGAGCGGACATTTAGAAAAAGAAATCAAAAGTCTCATGGAATATCAAAATCTTTCATTAAGTT 1020  
DB 8016 GGAGCGGACATTTAGAAAAAGAAATCAAAAGTCTCATGGAATATCAAAATCTTTCATTAAGTT 8075  
QY 1021 CGAGTTATTCAGATGGCCAAAGGAAAAATAAAGTCAATAGATAGAGTTGGTAGAATTTAG 1080  
DB 8076 CGAGTTATTCAGATGGCCAAAGGAAAAATAAAGTCAATAGATAGAGTTGGTAGAATTTAG 8135  
QY 1081 AACATGCTGTTTTCAGGTTTATGGTC-----TTTTTTTTTTTTTTTTTTTTTTTAAATAGGG 1135  
DB 8136 AACATGCTGTTTTCAGGTTTATGGTC-----TTTTTTTTTTTTTTTTTTTTTTTAAATAGGG 8195  
QY 1136 AAATGTGTTTGGTGAGAGCAATGTCAATCCAAAAGCTCTCTTTTCTGTCGTAGTC 1195  
DB 8196 AAATGTGTTTGGTGAGAGCAATGTCAATCCAAAAGCTCTCTTTTCTGTCGTAGTC 8255  
QY 1196 ATGTCCTGGGACAGAGAGGATCGGATTAGGCAACATCATAGAGTTGCTCTGAGCTGC 1255  
DB 8256 ATGTCCTGGGACAGAGAGGATCGGATTAGGCAACATCATAGAGTTGCTCTGAGCTGC 8315  
QY 1256 TCTTTGGTGATAACCTTTCCAAATCCTAAACTTTTGGAAATTCACAGCTCAAAAGGAGGA 1315  
DB 8316 TCTTTGGTGATAACCTTTCCAAATCCTAAACTTTTGGAAATTCACAGCTCAAAAGGAGGA 8375  
QY 1316 AACCTACTCTGATCTACACATGTTCTGCAATTTTCTATCATGTCATGGAACCTTC 1375  
DB 8376 AACCTACTCTGATCTACACATGTTCTGCAATTTTCTATCATGTCATGGAACCTTC 8435  
QY 1376 TCTTAGAATCCAGTGGCAAGAGTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 1435  
DB 8436 TCTTAGAATCCAGTGGCAAGAGTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 8495  
QY 1436 GTCATGAATCTCTGAGTATTTACTACTGATTTTGGGGGAGCTCAGCTATCGGTT 1495  
DB 8496 GTCATGAATCTCTGAGTATTTACTACTGATTTTGGGGGAGCTCAGCTATCGGTT 8555  
QY 1496 TCTTCACACCTGCTTATGAGAGTATCCATATTTATGTCGCGAGGCGAGTAATGCTCCCA 1555  
DB 8556 TCTTCACACCTGCTTATGAGAGTATCCATATTTATGTCGCGAGGCGAGTAATGCTCCCA 8614  
QY 1556 CGAGATCAGTTCTGAACTAACCTGGAAATTTTATGAGTTTATGAGTGGCACTATTA 1615  
DB 8615 CGAGATCAGTTCTGAACTAACCTGGAAATTTTATGAGTTTATGAGTGGCACTATTA 8674  
QY 1616 AATCAACATTCAGTTCTTCCCTCTGATTTCTCCTGTAAACATTAGGCTGCAAAAAA 1675  
DB 8675 AATCAACATTCAGTTCTTCCCTCTGATTTCTCCTGTAAACATTAGGCTGCAAAAAA 8734  
QY 1676 AAAAAATCTTTTAAAAATAATGCAATAAAGTATTTGCTCTGGGCTTACTGTATGCTC 1735  
DB 8735 AAAAAATCTTTTAAAAATAATGCAATAAAGTATTTGCTCTGGGCTTACTGTATGCTC 8794  
QY 1736 TTTTCTTTTCTCTTTTCAACTAAGTCACCGTCAATTTATTAAGTGGCCAACTAT 1795  
DB 8795 TTTTCTTTTCTCTTTTCAACTAAGTCACCGTCAATTTATTAAGTGGCCAACTAT 8854  
QY 1796 TCAAAACCTATGCTGAGTTCTTCAAGGAGGCTCACATAGTGATGAAGTTGGGATGGG 1855  
DB 8855 TCAAAACCTATGCTGAGTTCTTCAAGGAGGCTCGCATAGTGATGAAGTTGGGATGGG 8914  
QY 1856 CTACGGAGAAACCGAGCAACTCTAGTTTATTTAAACCTGTATTTACTGCCCACTTCC 1915  
DB 8915 CTACGGAGAAACCGAGCAACTCTAGTTTATTTAAACCTGTATTTACTGCCCACTTCC 8974  
QY 1916 CTTTAGACTTGAACATATGACCCCTCGCT-CCCATTTCTAAGCATAGGGGAGGCTTTATT 1974  
DB 8975 CTTTAGACTTGAACATATGACCCCTCGCT-CCCATTTCTAAGCATAGGGGAGGCTTTATT 9034  
QY 1975 TTTACATGGTAAATA---GATATCACTTGAGGTTTTATCAAAAGAGTTGCGGGGGTGGTG 2031

DB 9035 TTTCACATGGTAAATAGATGATATCATCTTGAGGTTTTATCAAGAGTTGCGGGGGTGGTG 9094  
QY 2032 AAAGTTCAACAACAGATTCAGGTTTTGTTGTGCCAGATTCATAATTTACATGTTCTTTT 2091  
DB 9095 AAAGTTCAACAACAGATTCAGGTTTTGTTGTGCCAGATTCATAATTTACATGTTCTTTT 9154  
QY 2092 TGCCAAAGGCTGATTTTTTTTAAATAAATGTTTCTCTTATCTTGTCTTTATTAGGTC 2151  
DB 9155 TGCCAAAGGCTGATTTTTTTTAAATAAATGTTTCTCTTATCTTGTCTTTATTAGGTC 9214  
QY 2152 GGAGACCATGAGAAACAGCGTCAAAATCATCTTTTATGATCCCAAGCTCAAAAGGCAAGCC 2211  
DB 9215 GGAGACCATGAGAAACAGCGTCAAAATCATCTTTTATGATCCCAAGCTCAAAAGGCAAGCC 9274  
QY 2212 CTCACAGAGCGTTATGTACCCACACACGAGCAATTTGGTCACAGACCTTCGGGGCCTG 2271  
DB 9275 CTCACAGAGCGTTATGTACCCACACGAGCAATTTGGTCACAGACCTTCGGGGCCTG 9334  
QY 2272 TCTGAAGCCATAGCTTCCACGGAGAGCCCT 2301  
DB 9335 TCTGAAGCCATAGCTTCCACGGAGAGCCCT 9364

RESULT 10  
ABZ96986  
ID ABZ96986 standard; DNA; 14879 BP.  
XX  
AC ABZ96986;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human nucleic acid sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
WP1; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 12228; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: the sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 14879 BP; 3971 A; 3370 C; 3434 G; 4103 T; 0 U; 1 Other;

Query Match 97.4%; Score 2241.6; DB 7; Length 14879;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 2294; Conservative 1; Mismatches 5; Indels 10; Gaps 4;

QY 1 CTGAATGATGCTCCCAAGTGTCTATGTGATGAGCTCCTTGTCGCCAGTGGGAATAGTG 60  
 DB 7056 CTGAATGATGCTCCCAAGTGTCTATGTGATGAGCTCCTTGTCGCCAGTGGGAATAGTG 7115

QY 61 TGTCATGTGCTATTTAAAGACTATTAATPACACTAATATAGTTTCTTCTCTTTGG 120  
 DB 7116 TGTCATGTGCTATTTAAAGACTATTAATPACACTAATATAGTTTCTTCTCTTTGG 7175

QY 121 ATATAGACGCTGTTCCGATGAGCTTGGAGCCCTAGTCCCAAGAGCCCTTGGAGA 180  
 DB 7176 ATATAGACGCTGTTCCGATGAGCTTGGAGCCCTAGTCCCAAGAGCCCTTGGAGA 7235

QY 181 ATTACTTCCCAAGGCAACAGACCGTGAATATAGATGCAATGCTAGTGCACAAAAG 240  
 DB 7236 ATTACTTCCCAAGGCAACAGACCGTGAATATAGATGCAATGCTAGTGCACAAAAG 7295

QY 241 ACAGAGTGTGGAATTTTGCACGAGCAAGAGAACTCAGGTGAGCAACACCTT 300  
 DB 7296 ACAGAGTGTGGAATTTTGCACGAGCAAGAGAACTCAGGTGAGCAACACCTT 7355

QY 301 TGCTTTTCAATCAGTTTAAACAGCTCCTGAACTCCTTCTATCATGTGCTGCTTCC 360  
 DB 7356 TGCTTTTCAATCAGTTTAAACAGCTCCTGAACTCCTTCTATCATGTGCTGCTTCC 7415

QY 361 TTTTAGAGACTAACAGAGACATTTGAAAGTCAAGGTAAGCTGAATATACATTTCTGA 420  
 DB 7416 TTTTAGAGACTAACAGAGACATTTGAAAGTCAAGGTAAGCTGAATATACATTTCTGA 7475

QY 421 AATGTTTTCTTGTGATTTTAAACAGGCTGAAGACATTTATGAGAAAGACTGGAAATA 480  
 DB 7476 AATGTTTTCTTGTGATTTTAAACAGGCTGAAGACATTTATGAGAAAGACTGGAAATA 7535

QY 481 TCATAAGAAAGAAAGACTCTTCAAGCTTGGGAAAGATGATTTATCAGCAGTTAGT 540  
 DB 7536 TCATAAGAAAGAAAGACTCTTCAAGCTTGGGAAAGATGATTTATCAGCAGTTAGT 7595

QY 541 GAGAGGAAGAAATCAGAGAGAGTTTACAGAGAACTTAAAGCAACACAGGTAAAGAGG 600  
 DB 7596 GAGAGGAAGAAATCAGAGAGAGTTTACAGAGAACTTAAAGCAACACAGGTAAAGAGG 7655

QY 601 AAGGAAGAAATATAGTGAAGAGTTTCAAGAAACAATAGCCCACTCAGTGAATGCCAG 660  
 DB 7656 AAGGAAGAAATATAGTGAAGAGTTTCAAGAAACAATAGCCCACTCAGTGAATGCCAG 7715

QY 661 CAGCTGTCTCCAGCCCTTCTTACCGGCGGCTGAAGACTTGAAGAACTAGAGTACAG 720  
 DB 7716 CAGCTGTCTCCAGCCCTTCTTACCGGCGGCTGAAGACTTGAAGAACTAGAGTACAG 7775

QY 721 AGGAGATCTATGCTCTATAGATTTAAAGAGCAAAAGAAATCCCTTTAAATATTCCA 780  
 DB 7776 AGGAGATCTATGCTCTATAGATTTAAAGAGCAAAAGAAATCCCTTTAAATATTCCA 7835

QY 781 TGAGCTCTGAAGTGAACCGAGTCTCTGTAATTTTGGACATACATTTTCATCTAC 840

DB 7836 TGAAGCTCTGGAATGCAAAACCGATCTCTCTACCTTTAGCACATACCAATTCATCTAC 7895

QY 841 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCTATGAGGTATATACAGC 900

DB 7896 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCTATGAGGTATATACAGC 7955

QY 901 CTTTGCTCTCTGAGTCAATGATTTTACACATTTCCCTGAGAAATCGAAATCATTTTGG 960

DB 7956 CTTTGCTCTCTGAGTCAATGATTTTACACATTTCCCTGAGAAATCGAAATCATTTTGG 8015

QY 961 GGAGCGGACATTTAGAAAAAGAAATCAAAAGTGTCTAGGTAATCAAAATCTTTCAATAGTT 1020

DB 8016 GGAGCGGACATTTAGAAAAAGAAATCAAAAGTGTCTAGGTAATCAAAATCTTTCAATAGTT 8075

QY 1021 GCAGTTATTCAGATGCCCAAGGAAATTAAGTCAATTAGATAGGTTGGTAGATTTAG 1080

DB 8076 GCAGTTATTCAGATGCCCAAGGAAATTAAGTCAATTAGATAGGTTGGTAGATTTAG 8135

QY 1081 AACATGCTCTTTTTCAGGTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 1135

DB 8136 AACATGCTCTTTTTCAGGTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 8195

QY 1136 AAATGTTTTGTTGAGAGCCCAATGTCATTTCCAAAAGCTCTCTTTTCTGCTGAGTGC 1195

DB 8196 AAATGTTTTGTTGAGAGCCCAATGTCATTTCCAAAAGCTCTCTTTTCTGCTGAGTGC 8255

QY 1196 ATGTGCTGGACAGAGAGGATCTGGATTAGGCAACATCATAGATTTGCTCTGAGCTGC 1255

DB 8256 ATGTGCTGGACAGAGAGGATCTGGATTAGGCAACATCATAGATTTGCTCTGAGCTGC 8315

QY 1256 TCTTTGGTGATTAACCTTCCAAATCCTAAACTTTTGGAAATTCACAACTCAAGAGGAGA 1315

DB 8316 TCTTTGGTGATTAACCTTCCAAATCCTAAACTTTTGGAAATTCACAACTCAAGAGGAGA 8375

QY 1316 AACCTACTCTCTGATCTACCATCTCTGCAATTTTCTATCATGCTCTATGGAACCTTC 1375

DB 8376 AACCTACTCTCTGATCTACCATCTCTGCAATTTTCTATCATGCTCTATGGAACCTTC 8435

QY 1376 TCTTAGAAATCCAGTGGCAAGATTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 1435

DB 8436 TCTTAGAAATCCAGTGGCAAGATTTCTATGATTAAGTGTCTGAGCTCAGGCCAGGCA 8495

QY 1436 GTCTAGAACTACTCTGAGTTTATTTACTACTGATTTGTTGGGCGAGCTCAGCTATCGTT 1495

DB 8496 GTCTAGAACTACTCTGAGTTTATTTACTACTGATTTGTTGGGCGAGCTCAGCTATCGTT 8555

QY 1496 TCTTCCACACCTCTGCTTATGAGAGTATCCATATTTATGTCGAGGCCAGTAATGTCCTCCA 1555

DB 8556 TCTTCCACACCTCTGCTTATGAGAGTATCCATATTTATGTCGAGGCCAGTAATGTCCTCCA 8614

QY 1556 CGAGATCAGTTTCTGAACTAACCTGGAAATTTTATGGGTTTTTATGTCGCACTATTA 1615

DB 8615 CGAGATCAGTTTCTGAACTAACCTGGAAATTTTATGGGTTTTTATGTCGCACTATTA 8674

QY 1616 AATCAACATTTACAGTTTCTTCTCTGATTTTCTCTGTAATAACATTTAGGCTCGCAAAAA 1675

DB 8675 AATCAACATTTACAGTTTCTTCTCTGATTTTCTCTGTAATAACATTTAGGCTCGCAAAAA 8734

QY 1676 AAAAAATCTTTTAAAAATATTTGCAATAAGTATTTGCTCTGGGCTCTGATGCTTC 1735

DB 8735 AAAAAATCTTTTAAAAATATTTGCAATAAGTATTTGCTCTGGGCTCTGATGCTTC 8794

QY 1736 TTTTCTTTTCTCTCTTTTCAACTAAGTCAAGTCAATTTTATTAAGATGGCCATAACTAT 1795

DB 8795 TTTTCTTTTCTCTCTTTTCAACTAAGTCAAGTCAATTTTATTAAGATGGCCATAACTAT 8854

QY 1796 TCAAAACCTATGCTGAGTTTCTCAAGGAGGCTCAGATGATGATGAGGTTGGATGGGG 1855

DB 8855 TCAAAACCTATGCTGAGTTTCTCAAGGAGGCTCAGATGATGATGAGGTTGGATGGGG 8914

QY 1856 CTACGGAAGAAACCAAGCAAACTCTAGTTTATTTAAAAACCTGTTTACTGCCCACTTCC 1915

DB 8915 CTACGGAAGAAACCAAGCAAACTCTAGTTTATTTAAAAACCTGTTTACTGCCCACTTCC 8974



FT exon /bound\_moiety= "Unspecified"  
 FT 9212..10443  
 FT \*tag= aa  
 FT protein\_bind 9392..9398  
 FT \*tag= ab  
 FT /bound\_moiety= "Unspecified"  
 FT protein\_bind 10751..10764  
 FT \*tag= ac  
 FT /bound\_moiety= "Unspecified"  
 XX  
 FN WO200222881-A1.  
 XX  
 FN 21-MAR-2002.  
 XX  
 PD 11-SEP-2001; 2001WO-US028834.  
 XX  
 PD 11-SEP-2000; 2000US-0231672P.  
 XX  
 PR 27-OCT-2000; 2000US-0243814P.  
 XX  
 XX (DZGE-) DZGENES LLC.  
 PA Moskowitz DW;  
 XX  
 PA WPI; 2002-393976/42.  
 XX  
 DR P-SDB; ABE14677.  
 XX  
 XX  
 PT Diagnosing genetic susceptibility for disease in a subject, by obtaining  
 PT a sample containing nucleic acid and detecting the presence/absence of a  
 PT single nucleotide polymorphism in the endothelin-1 gene.  
 XX  
 PS Claim 7; Page 72-81; 84pp; English.  
 XX  
 CC The invention relates to a method of diagnosing a genetic susceptibility  
 CC for a disease in a subject, involving obtaining a biological sample  
 CC containing nucleic acid from the subject, and analysing the nucleic acid  
 CC to detect a single nucleotide polymorphism (SNP) in the endothelin-1 (EDN  
 CC -1) gene, where the SNP is associated with a genetic predisposition for a  
 CC disease or a disorder. Examples of disorders include hypertension (HTN),  
 CC end stage renal disease (ESRD) due to HTN, non-insulin dependent diabetes  
 CC mellitus (NIDDM), ESRD due to NIDDM, lung cancer, breast cancer, prostate  
 CC cancer, colon cancer, atherosclerotic peripheral vascular disease (ASPWD)  
 CC due to HTN or NIDDM, cerebrovascular accident (CVA) due to HTN or NIDDM,  
 CC cataracts due to HTN, cardiomyopathy (CM) with HTN, myocardial infarction  
 CC (MI) due to HTN or NIDDM, ischaemic cardiomyopathy, ischaemic  
 CC cardiomyopathy with NIDDM, atrial fibrillation (afib) without valvular  
 CC disease, alcohol abuse, alcoholic cirrhosis, anxiety, asthma, chronic  
 CC obstructive pulmonary disease (COPD), cholecystectomy, degenerative joint  
 CC disease (DJD), ESRD and frequent de-clots, ESRD due to focal segmental  
 CC glomerular sclerosis (FSGS), and ESRD due to insulin dependent diabetes  
 CC mellitus (IDDM) or seizure disorder. The invention also provides a method  
 CC for treatment or prophylaxis of diseases associated with SNPs in  
 CC endothelin-1 gene. The present sequence is human endothelin-1 gene  
 CC containing SNPs in the promoter region  
 XX  
 SQ Sequence 12459 BP; 3372 A; 2727 C; 2816 G; 3543 T; 0 U; 1 Other;  
 Query Match 97.3%; Score 2239.6; DB 6; Length 12459;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 292; Conservative 1; Mismatches 5; Indels 10; Gaps 4;  
 QY 1 CTGAATGATGCTCCCAAGTCTATGTGATGAGTCCCTTGTGCCCAAGGAAATAGGTG 60  
 DB 7056 CTGAATGATGCTCCCAAGTCTATGTGATGAGTCCCTTGTGCCCAAGGAAATAGGTG 7115  
 QY 61 TGTCCATGTCATTTAAAGACTATTAATACACTAATAGTTCTTCTCTCTTTGG 120  
 DB 7116 TGTCCATGTCATTTAAAGACTATTAATACACTAATAGTTCTTCTCTCTTTGG 7175  
 QY 121 ATAATAGGACGTTGTTCCGATGGACTTGAAGCCCTTAGTCCCAAGAGAGCCCTTGAGA 180  
 DB 7176 ATAATAGGACGTTGTTCCGATGGACTTGAAGCCCTTAGTCCCAAGAGAGCCCTTGAGA 7235  
 QY 181 ATTACTTCCCAAGGACACACCGGTGAATAATAGATGCCAATGTGCTAGCCAAAAG 240

DB 7236 ATTTACTTCCCAAGGCAACAGACCGTGAATAGATGCCAATGTGCTAGCCAAAAG 7295  
 QY 241 ACAAGAGTGTGGAAATTTTGGCCAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 300  
 DB 7296 ACAAGAGTGTGGAAATTTTGGCCAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 7355  
 QY 301 TGCCTTTCAATCAGTTTAAACAGCCTCCTGAACTCCTTCTCTATCATGCTGCTCTCTG 360  
 DB 7356 TGCCTTTCAATCAGTTTAAACAGCCTCCTGAACTCCTTCTCTATCATGCTGCTCTCTG 7415  
 QY 361 TTTTAGAGAGCTAAACAGAGACATTTGAAAGTCAGGTAAGCTGAATATAACATTTGCTGA 420  
 DB 7416 TTTTAGAGAGCTAAACAGAGACATTTGAAAGTCAGGTAAGCTGAATATAACATTTGCTGA 7475  
 QY 421 AATGTTTTTCTTGTGTATTTTAAACAGGCTCAAGACATTTATGGAGAAGACTGGAATAA 480  
 DB 7476 AATGTTTTTCTTGTGTATTTTAAACAGGCTCAAGACATTTATGGAGAAGACTGGAATAA 7535  
 QY 481 TCATAAGAAAGGAAAGACTGTTTCAAGCTTCGGAAAGTGTATTTATCAGCAGTTAGT 540  
 DB 7536 TCATAAGAAAGGAAAGACTGTTTCAAGCTTCGGAAAGTGTATTTATCAGCAGTTAGT 7595  
 QY 541 GAGAGGAAAGAAATCAGAAAGTTCAGAGGAAACACCTAAGACAAACAGGTAGAGGG 600  
 DB 7596 GAGAGGAAAGAAATCAGAAAGTTCAGAGGAAACACCTAAGACAAACAGGTAGAGGG 7655  
 QY 601 AAGGAAGAAATTTAGTAAAGAGTTTCAAGAACTAGTCCCGCAGTCAGTATGCCAG 660  
 DB 7656 AAGGAAGAAATTTAGTAAAGAGTTTCAAGAACTAGTCCCGCAGTCAGTATGCCAG 7715  
 QY 661 CAGCCTGTTCTCCAGCCCTTCTTACCCTGGGAGTGAAGAACTTAGAAAACAGTAGCAG 720  
 DB 7716 CAGCCTGTTCTCCAGCCCTTCTTACCCTGGGAGTGAAGAACTTAGAAAACAGTAGCAG 7775  
 QY 721 AGGAGATCTATCATCTTATAGATTAAGAGGAGAAAGAAATCCCTCTTAATAATTTCCA 780  
 DB 7776 AGGAGATCTATCATCTTATAGATTAAGAGGAGAAAGAAATCCCTCTTAATAATTTCCA 7835  
 QY 781 TGAAGCTCTGGAATCAAAACCGATGCTCTCTGTACTTTTAGCACATACCATTTCTAC 840  
 DB 7836 TGAAGCTCTGGAATCAAAACCGATGCTCTCTGTACTTTTAGCACATACCATTTCTAC 7895  
 QY 841 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTGTTCATTTGGTATATACAGC 900  
 DB 7896 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTGTTCATTTGGTATATACAGC 7955  
 QY 901 CTTTGGCTCTCTGAGTCAATGATTTTACACCTTCCCTCGAGAAATCGAAAATCATTTTGG 960  
 DB 7956 CTTTGGCTCTCTGAGTCAATGATTTTACACCTTCCCTCGAGAAATCGAAAATCATTTTGG 8015  
 QY 961 GGAGCGGACATTTAGAAAAGAAATCAAGTGTCTAGGATTAATCAAAATTTCTCAATAAGTT 1020  
 DB 8016 GGAGCGGACATTTAGAAAAGAAATCAAGTGTCTAGGATTAATCAAAATTTCTCAATAAGTT 8075  
 QY 1021 GCAGTTATTTACATGCCCAAGGAAATTAAGTCAATTAGATAGGTTGGTAGAATTTAG 1080  
 DB 8076 GCAGTTATTTACATGCCCAAGGAAATTAAGTCAATTAGATAGGTTGGTAGAATTTAG 8135  
 QY 1081 AACATGCTGTTTTTCAAGTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 1135  
 DB 8136 AACATGCTGTTTTTCAAGTTTATGTC-----TTTTTTTTTTTTTTTTTTTTTAAATAGGG 8195  
 QY 1136 AAATGTTTTTGTGAGAGCCCAATGCTCATTCAAAAAGCTCTCTTTTCTGGTTCAGTC 1195  
 DB 8196 AAATGTTTTTGTGAGAGCCCAATGCTCATTCAAAAAGCTCTCTTTTCTGGTTCAGTC 8255  
 QY 1196 ATGCTGTGGACAGAGAGGATCTGGATTTAGGCAACATCATAGAGTTGCTCTGAGTGC 1255  
 DB 8256 ATGCTGTGGACAGAGAGGATCTGGATTTAGGCAACATCATAGAGTTGCTCTGAGTGC 8315  
 QY 1256 TCTTTGGTGATACCCCTTCCAAATCCTTAACTTTTGAATTCACAACTCAAGTCAGAGGAGA 1315

Db 8316 TCTTTGGTGATAACCCCTTCCAAATCCTAAATCTTGGAAATTCACAAGCTCAAGAGGA 8375  
Qy 1316 AACCTACTCTGATCTACACATGTTCTGCAATTTTCTATCATGCTCTATGGAACCTC 1375  
Db 8376 AACCTACTCTGATCTACACATGTTCTGCAATTTTCTATCATGCTCTATGGAACCTC 8435  
Qy 1376 TCTTAGAATCCAGTGGCAGAGTTCTATGATTAAGAGTTCTGAGCTCAGGCCAGCA 1435  
Db 8436 TCTTAGAATCCAGTGGCAGAGTTCTATGATTAAGAGTTCTGAGCTCAGGCCAGCA 8495  
Qy 1436 GTCATGAATCTCTGAGTTATTTACTACTGATTTGTTGGGCGAGCTCAGTATCGTT 1495  
Db 8496 GTCATGAATCTCTGAGTTATTTACTACTGATTTGTTGGGCGAGCTCAGTATCGTT 8555  
Qy 1496 TCTTCACACCTGTTATGAGAGTATCCATATTTATGGTCCGAGGCGAGTAATGCTCCCA 1555  
Db 8556 TCTTCACACCTGTTATGAGAGTATCCATATTTATGGTCCGAGG-CAGTAATGCTCCCA 8614  
Qy 1556 CGAGATCAGTTCTGAACTAACTGGAATTTTATGAGTTTATGAGTTTATGCAACTATTA 1615  
Db 8615 CGAGATCAGTTCTGAACTAACTGGAATTTTATGAGTTTATGAGTTTATGCAACTATTA 8674  
Qy 1616 AATCAACATTACAGTTCTTCCCTCTGTTTCTCTGTAAGAACTATGAGCTGCAAAAA 1675  
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Qy 1676 AAAAAATCTTTTAAAAATTAATGCAATAAGTATTTGCTGCGGCTACTGATGCTTC 1735  
Db 8735 AAAAAATCTTTTAAAAATTAATGCAATAAGTATTTGCTGCGGCTACTGATGCTTC 8794  
Qy 1736 TTTTCTTTTCTCTCTTTTCACTAAGTACCGTCAATTTATAGATGGCCATCACTAT 1795  
Db 8795 TTTTCTTTTCTCTCTTTTCACTAAGTACCGTCAATTTATAGATGGCCATCACTAT 8854  
Qy 1796 TCAAAACCTATGCTGAGTTCTTCAAGGCGAGGTCACATAGTATGATGAAGTTGGATGGG 1855  
Db 8855 TCAAAACCTATGCTGAGTTCTTCAAGGCGAGGTCGATAGTATGATGAAGTTGGATGGG 8914  
Qy 1856 CTACGGAAGAACCAAGCACTGATGTTATTTAAACCTGATTTACTGCGCACTTCC 1915  
Db 8915 CTACGGAAGAACCAAGCACTGATGTTATTTAAACCTGATTTACTGCGCACTTCC 8974  
Qy 1916 CCTTAGACTTGACCATATGACCCCTCGCT-CCCATTTCAAGCATAGGGCGAGCTTTAT 1974  
Db 8975 CCTTAGACTTGACCATATGACCCCTCGCTCCCATTTCAAGCATAGGGCGAGCTTTAT 9034  
Qy 1975 TTTAATGGTAATA---GATATCACTGAGTTTATCAAGAGTTGCGGGGGTGGTG 2031  
Db 9035 TTTAATGGTAATAGATATCACTGAGTTTATCAAGAGTTGCGGGGGTGGTG 9094  
Qy 2032 AAGTTTCAACACAGATTCAGTTTGTGTCAGATTTCTAATTTTACATGTTCTTT 2091  
Db 9095 AAGTTTCAACACAGATTCAGTTTGTGTCAGATTTCTAATTTTACATGTTCTTT 9154  
Qy 2092 TGCCAAAGGGTGATTTTTTAAATAACATTTGTTTCTCTTATCTTGCTTTTATGATC 2151  
Db 9155 TGCCAAAGGGTGATTTTTTAAATAACATTTGTTTCTCTTATCTTGCTTTTATGATC 9214  
Qy 2152 GGNAGCATGAGAACAGCGTCAATCTTTTCTATGATCCAGCTGAGAGGCAAGCC 2211  
Db 9215 GGNAGCATGAGAACAGCGTCAATCTTTTCTATGATCCAGCTGAGAGGCAAGCC 9274  
Qy 2212 CTCGAGAGCGTTATGTCACCCACACAGCGATTTGGTGACAGACCTTCGGGGCCTG 2271  
Db 9275 CTCGAGAGCGTTATGTCACCCACACAGCGATTTGGTGACAGACCTTCGGGGCCTG 9334  
Qy 2272 TCTGAAGCCATAGCTCCAGGAGGCC 2299  
Db 9335 TCTGAAGCCATAGCTCCAGGAGGCC 9362

RESULT 12  
ABV76130

ID AVB76130 standard; cDNA; 1250 BP.  
XX AC AVB76130;  
XX DT 07-MAR-2003 (first entry)  
XX DE Human endothelin-1 nucleic acid.  
XX DE DE Gene therapy; vector; hepatitis B virus; cardiovascular disease; heart;  
KW KW cardiant; vasotropic; antiarrhythmic; antiarteriosclerotic; human;  
KW KW endothelin-1; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200287594-A1.  
XX PD 07-NOV-2002.  
XX PF 30-APR-2002; 2002WO-US013644.  
XX PR 30-APR-2001; 2001US-0287423P.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PI Chien KR, Hoshijima M;  
XX DR WPI; 2003-111844/10.  
XX PT Novel non-viral vector comprises vesicular membrane with hepatitis B  
PT PT envelope protein with cardiac targeting sequence, and nucleotide sequence  
PT PT for gene therapy useful for treating, e.g., heart failure, arrhythmia and  
XX XX atherosclerosis.  
PS Disclosure; Page 21-22; 53pp; English.  
XX XX The present sequence is that of a human endothelin-1 nucleic acid. The  
CC CC invention provides a non-viral vesicle vector for the delivery of nucleic  
CC CC acid to various cardiac cell types. The vesicle vector contains the  
CC CC hepatitis B virus envelope protein in which at least part of the liver  
CC CC targeting sequence is deleted and replaced with a specific cardiac cell  
CC CC which is used to broadly target the cardiovascular system. The vesicle  
CC CC vector can be delivered intravenously or intra-arterially rather than by  
CC CC more invasive methods such as direct cardiac injection. It can be used to  
CC CC deliver gene products to replace or enhance expression of proteins for  
CC CC treatment of heart failure, arrhythmia, reperfusion injury, etc.  
CC CC atherosclerosis, to promote angiogenesis, etc. The vesicles are highly  
CC CC stable and can be produced in large quantities, making them ideal for  
XX XX gene therapy  
SQ Sequence 1250 BP; 312 A; 332 C; 318 G; 288 T; 0 U; 0 Other;  
Query Match 6.9%; Score 159; DB 7; Length 1250;  
Best Local Similarity 97.0%; Pred. No. 2.7e-27;  
Matches 162; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 128 GCACGTTGTTCCGTTATGGACTTGAAGCCCTAGTCCAGAGAGCCCTTGGAGATTACT 187  
Db 568 GCACGTTGTTCCGTTATGGACTTGAAGCCCTAGTCCAGAGAGCCCTTGGAGATTACT 627  
Qy 188 TCCACAAAGGCAACAGACCGTGAAATAGATGCAATGTCTAGCCAAAAGACACAA 247  
Db 628 TCCACAAAGGCAACAGACCGTGAAATAGATGCAATGTCTAGCCAAAAGACACAA 687  
Qy 248 GTGCTGGAATTTTCCCAAGCAGGAAAAGAACTCAGGTGAGCAGAAA 294  
Db 688 GTGCTGGAATTTTCCCAAGCAGGAAAAGAACTCAGGTGAGCAGAAA 734  
RESULT 13  
AAH48266  
ID AAH48266 standard; DNA; 636 BP.  
XX XX

AC AAH48266;  
 XX 21-SEP-2001 (first entry)  
 XX Heart muscle cell differentiation related DNA SEQ ID NO: 66.  
 DE Heart muscle cell; human; cell differentiation; heart disease; ds.  
 KW Heart muscle cell; human; cell differentiation; heart disease; ds.  
 XX Homo sapiens.  
 OS WO200148151-A1.  
 PN 05-JUL-2001.  
 PD 27-DEC-2000; 2000WO-JP009323.  
 XX 28-DEC-1999; 99JP-00372826.  
 PR 28-FEB-2000; 2000WO-JP001148.  
 PR 02-NOV-2000; 2000WO-JP007741.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;  
 PI Yamada Y;  
 XX WPI: 2001-425656/45.  
 DR P-PSDB; AAG64862.  
 XX Cells capable of differentiating into cardiomyocytes and originating in  
 PT bone marrow or umbilical blood cells for study of cardiomyocyte  
 PT differentiation and treatment of heart disease.  
 XX Claim 32; Page 168-170; 183pp; Japanese.  
 XX The present invention provides cells originating in the human bone marrow  
 CC or umbilical blood cells which are capable of differentiating into  
 CC cardiomyocytes. These cells are useful in the treatment of diseases  
 CC involving heart muscle degeneration, such as myocardial infarction, and  
 CC the study of cardiomyocyte differentiation. The present sequence is an  
 CC oligonucleotide described in the exemplification of the invention  
 XX Sequence 636 BP; 191 A; 147 C; 165 G; 133 T; 0 U; 0 Other;  
 SQ Query Match 6.8%; Score 157.4; DB 4; Length 636;  
 Best Local Similarity 96.4%; Pred. No. 5.1e-27;  
 Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 128 GCACGTTGTCGTTAGCTTGGAGCCCTAGGTCCAGAGAGCCCTGGAGATTACT 187  
 Db 234 GCACGTTGTCGTTAGCTTGGAGCCCTAGGTCCAGAGAGCCCTGGAGATTACT 293  
 QY 188 TCCCAAGGCAACAGACCCGTCGTAATAGATGCCAATGTGCTAGCCAAAGCAAGAA 247  
 Db 294 TCCCAAGGCAACAGACCCGTCGTAATAGATGCCAATGTGCTAGCCAAAGCAAGAA 353  
 QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACGAGAA 294  
 Db 354 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACGAGAA 400  
 RESULT 14  
 AAH44397  
 ID AAH44397 standard; cDNA; 636 BP.  
 XX AAH44397;  
 XX 26-SEP-2001 (first entry)  
 XX Human ET1 nucleotide sequence SEQ ID NO:66.  
 DE Differentiation; heart muscle cell; cytokine; transcription factor;  
 KW proliferation; surface antigen; heart disease; cardiomyocyte;  
 KW bone marrow; umbilical blood cell; heart muscle degeneration;

KW myocardial infarction; ss.  
 XX Homo sapiens.  
 PN WO200148150-A1.  
 XX 05-JUL-2001.  
 PD 02-NOV-2000; 2000WO-JP007741.  
 XX 28-DEC-1999; 99JP-00372826.  
 PR 28-FEB-2000; 2000WO-JP001148.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;  
 PI Yamada Y;  
 XX WPI: 2001-425655/45.  
 DR P-PSDB; AAB99933.  
 XX Cells capable of differentiating into cardiomyocytes and originating in  
 PT bone marrow or umbilical blood cells for study of cardiomyocyte  
 PT differentiation and treatment of heart disease.  
 XX Claim 32; Page 162-164; 187pp; Japanese.  
 XX The present invention describes cells originating in bone marrow or  
 CC umbilical blood cells which are capable of differentiating into  
 CC cardiomyocytes. Also described are: (1) cardiomyocytes produced by the  
 CC differentiation of the cells; (2) a method for carrying out the  
 CC differentiation into cardiomyocytes, regulated by a promotonal and/or  
 CC inhibitory factor; (3) a method for the differentiation of the cells into  
 CC cell types other than cardiomyocytes; (4) drug compositions promoting the  
 CC formation of heart muscle and regeneration of heart tissue which contain  
 CC the cells; (5) a method for the production of antibodies which recognise  
 CC the cells, especially antibodies which recognise a surface antigen on the  
 CC cells; (6) a method for screening factors which promote the proliferation  
 CC of the cells; (7) a method for immortalising the cells by expressing  
 CC telomerase in them; (8) drug compositions for the treatment of heart  
 CC disease which contain the immortalised cells; and (9) cell-free  
 CC supernatant from the culture of the cells and its use in promoting their  
 CC differentiation into cardiomyocytes. The cells are used in the treatment  
 CC of diseases involving heart muscle degeneration, such as myocardial  
 CC infarction and in the study of cardiomyocyte differentiation. AAH44351 to  
 CC AAH44409 and AAB99915 to AAB99935 represent sequences used in the  
 CC exemplification of the present invention  
 XX Sequence 636 BP; 191 A; 147 C; 165 G; 133 T; 0 U; 0 Other;  
 SQ Query Match 6.8%; Score 157.4; DB 4; Length 636;  
 Best Local Similarity 96.4%; Pred. No. 5.1e-27;  
 Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 128 GCACGTTGTCGTTAGCTTGGAGCCCTAGGTCCAGAGAGCCCTGGAGATTACT 187  
 Db 234 GCACGTTGTCGTTAGCTTGGAGCCCTAGGTCCAGAGAGCCCTGGAGATTACT 293  
 QY 188 TCCCAAGGCAACAGACCCGTCGTAATAGATGCCAATGTGCTAGCCAAAGCAAGAA 247  
 Db 294 TCCCAAGGCAACAGACCCGTCGTAATAGATGCCAATGTGCTAGCCAAAGCAAGAA 353  
 QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACGAGAA 294  
 Db 354 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGACGAGAA 400  
 RESULT 15  
 AAH35169  
 ID AAH35169 standard; DNA; 1167 BP.  
 XX AAH35169;  
 XX

DT 28-JUL-2000 (first entry)  
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:43.  
DE  
XX  
KW Human; adenosine receptor; low adenosine antisenase oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200009525-A2.  
PN  
XX  
XX 24-FEB-2000.  
PD  
XX  
XX 03-AUG-1999; 99WO-US017712.  
PF  
XX  
PR 03-AUG-1998; 98US-0095212P.  
PR  
XX (UYEC-) UNIV EAST CAROLINA.  
PA  
XX  
XX Nyce JW;  
PI  
XX WPI; 2000-205971/18.  
DR  
XX  
XX New antisenase oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
PT  
XX  
PS Disclosure; Page 1201; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisenase  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 1167 BP; 288 A; 309 C; 299 G; 271 T; 0 U; 0 Other;

Query Match 6.8%; Score 157.4; DB 3; Length 1167;  
Best Local Similarity 96.4%; Pred. No. 6.3e-27;  
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 GCACGTTGTTCCCGTATGGACTTGAAGCCCTAGTCCCAAGAGAGCCCTGGAGAAATTACT 187  
|||||  
Db 486 GCACGTTGTTCCCGTATGGACTTGAAGCCCTAGTCCCAAGAGAGCCCTGGAGAAATTACT 545  
|||||

QY 188 TCCCAAGAGGCAACAGACCGTGAAATAGATGCCAATGTGCTAGCCAAAAGACAGAA 247  
|||||

Db 546 TCCCAAGAGGCAACAGACCGTGAGAAATAGATGCCAATGTGCTAGCCAAAAGACAGAA 605  
QY 248 GTGCTGGAATTTTGGCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 294  
Db 606 GTGCTGGAATTTTGGCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 652

Search completed: July 16, 2004, 15:57:05  
Job time : 875 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2004, 15:07:49 ; Search time 162 Seconds  
(without alignments)  
7882.358 Million cell updates/sec

Title: US-10-043-715-1\_COPY\_157700\_160000

Perfect score: 2301

Sequence: 1 ctgaatgatgtcccaagt.....tagctccacggagagccct 2301

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
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3: /cgn2\_6/ptodata/2/ina/5A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	66.6	2.9	7218	1 US-08-232-463-14	Sequence 14, Appl
C 2	45.2	2.0	223	4 US-09-621-976-10791	Sequence 10791, A
C 3	45.2	2.0	5152	4 US-10-204-708-48	Sequence 48, Appl
C 4	44.4	1.9	832	4 US-09-621-976-2813	Sequence 2813, Ap
C 5	43.6	1.9	5501	4 US-10-204-708-38	Sequence 38, Appl
C 6	42.8	1.9	7218	1 US-08-232-463-14	Sequence 14, Appl
C 7	42.4	1.8	1492	4 US-09-369-247-23	Sequence 23, Appl
C 8	42	1.8	2668	4 US-09-370-838-156	Sequence 156, App
C 9	41.6	1.8	4597	4 US-08-961-527-175	Sequence 175, App
C 10	40.4	1.8	9347	4 US-10-204-708-35	Sequence 35, Appl
C 11	40.2	1.7	5152	4 US-10-204-708-73	Sequence 73, Appl
C 12	39.6	1.7	535	4 US-09-621-976-2255	Sequence 2255, Ap
C 13	39.6	1.7	5501	4 US-10-204-708-37	Sequence 37, Appl
C 14	39.4	1.7	6306	4 US-10-204-708-50	Sequence 50, Appl
C 15	39	1.7	8093	4 US-10-204-708-32	Sequence 32, Appl
C 16	39	1.7	11049	4 US-10-204-708-23	Sequence 23, Appl
C 17	38.8	1.7	3394	4 US-09-738-946-7	Sequence 7, Appl
C 18	38.6	1.7	586	3 US-09-134-000C-1689	Sequence 366, App
C 19	38.4	1.7	2148	4 US-09-621-976-18033	Sequence 1689, Ap
C 20	38.4	1.7	640681	4 US-09-790-988-1	Sequence 1, Appl
C 21	38.2	1.7	474	4 US-09-621-976-18033	Sequence 18033, A
C 22	38.2	1.7	853	3 US-09-174-768-5	Sequence 5, Appl
C 23	38.2	1.7	1353	4 US-08-956-171E-521	Sequence 521, App
C 24	38.2	1.7	786431	4 US-09-751-389-3	Sequence 3, Appl
C 25	38	1.7	1945	3 US-08-714-918-77	Sequence 77, Appl
C 26	38	1.7	1945	3 US-09-265-315-77	Sequence 77, Appl
C 27	38	1.7	1945	3 US-09-265-315-77	Sequence 77, Appl

Query Match 2.9%; Score 66.6; DB 1; Length 7218;

## ALIGNMENTS

### RESULT 1

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)883-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: ptz9pt-F1s

; US-08-232-463-14

[illegible]

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RESULT 2
US-09-621-976-10791/c
; Sequence 10791, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10791
; LENGTH: 223
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-10791

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Query Match      2.0%;   Score 45.2;   DB 4;   Length 223;
Best Local Similarity 54.1%;   Pred. No. 0.027;
Matches 92;   Conservative 0;   Mismatches 78;   Indels 0;   Gaps 0;

QY      1090  TTTTTCAGGTTTATGGTCTTTTTTTTTTTTTTTTTTAAATAGGAAATGTGTTGGTG 1149
          |||||
Db       222  TTTTTCAGGTTTATGGTCTTTTTTTTTTTTTTTTTTAAATAGGAAATGTGTTGGTG 163
          |||||

QY      1150  CAGAGCGAATGTCATTCACAAAAGCTCTCTTTTCTCGTCTAGTCATGCTGCGGACAG 1209
          |||||
Db       162  TACAAAATAATGACAAATATATTTCTCTTATGTTCTCATCTCGGCTGTGTCAGGGGTT 103
          |||||

QY      1210  AGAAGGATCTGGATAGGCAACATAGAGTTGCTCTCAGCTGCTCTT 1259
          |||||
Db       102  AGTAGTCTGTATTTGTGTATTTAAAAAAATAGTCATCGTCTCTT 53
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RESULT 3
US-10-204-708-48
; Sequence 48, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: REELIN, Kurt

```

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; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
; US-09-621-976-2813

Query Match      1.9%; Score 44.4; DB 4; Length 832;
Best Local Similarity 14.1%; Pred. No. 0.077;
Matches 54; Conservative 156; Mismatches 172; Indels 0; Gaps 0;

992 TCATGGATATCAAAATTCCTCAATAAGTTCGAGTTATTCAGATGCCCAAGGAAAAATAA 1051

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[illegible]

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RESULT 10
US-10-204-708-35
; Sequence 35, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 35
; LENGTH: 9347
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

```

	Query Match	1.8%;	Score 40.4;	DB 4;	Length 9347;
	Best Local Similarity	55.8%;	Pred. No. 2.3;		
	Matches 77;	Conservative 0;	Mismatches 61;	Indels 0;	Gaps 0;
QY	990	TGTCATGGATAATCAAAATCTTC	AAATAGTTGCAGTTATT	CAGATGCCAAAGSAAAAAT	1049
Db	5856	TGTTTTAAATTTTAAATTTTGAATTTTTT	TATATATAAAAGATAACGAACGTTAATTT		5915
QY	1050	AAAGTCATTAGATAGGGTTGGTAGAAATTTAGAACATGCTGTTTTTC	CAGTTTTCAGGTTTATGCGTCMT		1109
Db	5916	TATGTTGACAAATTTTTTTT	TAGAAATTTAGAAATATTTTAAAGTTTTTATGTTTAGTGTTTTTT		5975
QY	1110	TTTTTTTTTTTTTTTTTTTT		1127	
Db	5976	TTTTTTTTTTTTTTTTTTTT		5993	

RESULT 11  
US 5107-204-708-73  
; Request No. 73, Application US/10204708  
; Request No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt

```

, TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
,
, TITLE OF INVENTION: by Assessing DNA Methylation
,
, FILE REFERENCE: 5013.1012
,
, CURRENT APPLICATION NUMBER: US/10/204,708
,
, CURRENT FILING DATE: 2003-05-06
,
, PRIOR APPLICATION NUMBER: PCT/EP01/03971
,
, PRIOR FILING DATE: 2001-04-06
,
, PRIOR APPLICATION NUMBER: DE 10019058.8
,
, PRIOR FILING DATE: 2000-04-06
,
, PRIOR APPLICATION NUMBER: DE 10019173.8
,
, PRIOR FILING DATE: 2000-04-07
,
, PRIOR APPLICATION NUMBER: DE 10032529.7
,
, PRIOR FILING DATE: 2000-06-30
,
, PRIOR APPLICATION NUMBER: DE 10043826.1
,
, PRIOR FILING DATE: 2000-09-01
,
, NUMBER OF SEQ ID NOS: 98
,
, SEQ ID NO 73
,
, LENGTH: 5152
,
, TYPE: DNA
,
, ORGANISM: Artificial Sequence
,
, FEATURE:
,
, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
,
, US-10-204-708-73

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	Query Match	1.7%	Score 40.2;	DB 4;	Length 5152;
	Best Local Similarity 52.0%;	Pred. No. 2;			
	Matches 90;	Conservative	0;	Mismatches 83;	Indels 0;
	Gaps 0;				
Qy	973	TAGAAAAGAATCAAAAGTGT	CATGGATAATCAAAATCTT	CAATAAGCTGCAGTATTTCAG	1032
Db	2387	TAGAGAGAGATTTTGT	TTTTTAAATTTAGTTAAATAATAATTAATTTTAAATAATTAA	2446	
Qy	1033	ATGCCCAAGCAAAAAATAAAGT	CATTAGATPAGGGTTGGT	TAGAAATTTAGAACATCGTGT	1092
Db	2447	AAAAAAAATAAAATTTTGT	TTTTTTATTTGGTTTTTAGAATAAATAATAAAATAGGAAGT	2506	
Qy	1093	TTCAGGTTTATGGTCT	TTTTTTTTTTTTTTTTTTTTTTTTTTTAAATAGGGAATGCTTT	1145	
Db	2507	TTGTTATTTTTTGGGTTTTT	TTAGTGTGTTATTTT	TTTTTTTTTTTGTAGTATGSGTTT	2559

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RESULT 12
US-09-621-976-2255/c
; Sequence 2255, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joberit, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2255
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..385
US-09-621-976-2255

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	Query Match	1.7%	Score 39.6	DB 4	Length 535
	Best Local Similarity	63.8%	Pred. No. 1.1		
	Matches 60	Conservative 5	Indels 34	Gaps 0	
QY	531	AGCAGTTAGTCAGAGGAGAAAAATTCAGAGAGTTCACGAGACACCTACAGACCA	590		
DB	161	AGGAAATTTGCAAGCGTAGAAAAATGGAGAAAAAAGGAAACATAAAGGAGATT	102		
QY	591	GCTACAGCGGAGGAGAGAAAAATTAGGTAAGAGG	624		



Mon Jul 19 16:14:28 2004

us-10-043-715-1\_copy\_157700\_160000.rni

Page 7

Search completed: July 16, 2004, 17:36:50  
Job time : 165 secs

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2	727.4	31.6	1339	13	US-10-037-632-124859	Sequence 124859,
3	727.4	31.6	1339	16	US-10-037-632-124859	Sequence 124859,
4	159	6.9	1350	15	US-10-136-619-3	Sequence 3, Appli
5	157.4	6.8	1356	9	US-09-749-738B-66	Sequence 66, Appli
6	157.4	6.8	1166	15	US-10-295-942-1	Sequence 1, Appli
7	157.4	6.8	1251	13	US-10-211-462-126	Sequence 126, App
8	157.4	6.8	1251	13	US-10-342-987-701	Sequence 701, App
9	157.4	6.8	1251	13	US-10-172-118-701	Sequence 701, App
10	157.4	6.8	1251	13	US-10-170-385-398	Sequence 398, App
11	157.4	6.8	1251	15	US-10-007-926A-458	Sequence 458, App
12	157.4	6.8	1251	15	US-10-101-510-5	Sequence 5, Appli
13	157.4	6.8	1251	15	US-10-031-660-40	Sequence 40, Appli
14	156.4	6.8	1566	15	US-10-060-036-22	Sequence 22, Appli

Db 157880 ATTACTTCCCAAGGCAACAGACCGGTGAAAATAGATGCCAATGTGCTAGCCAAAAG 157939  
QY 241 ACAAGAGTGTGGAAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 300  
Db 157940 ACAAGAGTGTGGAAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 157999  
QY 301 TGCCTTTCAATCAGTTTAAACAGCCTCCTGAACTCCTTCTCTATCATGGTACTGCCTTCC 360  
Db 158000 TGCCTTTCAATCAGTTTAAACAGCCTCCTGAACTCCTTCTCTATCATGGTACTGCCTTCC 158059  
QY 361 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGGTAAAGCTGAATTAACATTTGCTGA 420  
Db 158060 TTTTAGAGAGACTAACAGAGACATTTGAAAGTCAGGGTAAAGCTGAATTAACATTTGCTGA 158119  
QY 421 AATGTTTTTCCCTGTGTATTTTAAACAGGGCTGAAGACATTTAGGAGAAAGACTGGAATAA 480  
Db 158120 AATGTTTTTCCCTGTGTATTTTAAACAGGGCTGAAGACATTTAGGAGAAAGACTGGAATAA 158179  
QY 481 TCATTAAGAAAGAAAGACTGTTCOAAGCTTGGGAAAAGTGTATTTATCAGCAGTTAGT 540  
Db 158180 TCATTAAGAAAGAAAGACTGTTCOAAGCTTGGGAAAAGTGTATTTATCAGCAGTTAGT 158239  
QY 541 GAGAGAGAAAGAAATCAGAAAGTTCAGAGAAACACCTTAAGACAAACACAGGTAAAGGG 600  
Db 158240 GAGAGAGAAAGAAATCAGAAAGTTCAGAGAAACACCTTAAGACAAACACAGGTAAAGGG 158299  
QY 601 AAGGAGAAAGAAATTAAGTAAAGAGTTTCAAGAAACAACTAGCCCCAGTCAGTATGCCAG 660  
Db 158300 AAGGAGAAAGAAATTAAGTAAAGAGTTTCAAGAAACAACTAGCCCCAGTCAGTATGCCAG 158359  
QY 661 CAGCCTGTTCCTCCAGCCCTTCTTACCGGCGAGGTGAAAGACTTGAAGAAACAGTAGCAG 720  
Db 158360 CAGCCTGTTCCTCCAGCCCTTCTTACCGGCGAGGTGAAAGACTTGAAGAAACAGTAGCAG 158419  
QY 721 AGGAGATCTATGATCTCTATAGATTAAAGAGGAGCAAGAAAGATCCCTCTTAAATATTTCCA 780  
Db 158420 AGGAGATCTATGATCTCTATAGATTAAAGAGGAGCAAGAAAGATCCCTCTTAAATATTTCCA 158479  
QY 781 TGAAGCTCTGAAATGCAACCGATGTCTCTGTACTTTTACGACATACCAATTCATCTAC 840  
Db 158480 TGAAGCTCTGAAATGCAACCGATGTCTCTGTACTTTTACGACATACCAATTCATCTAC 158539  
QY 841 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCAATGGGTTATATACAGC 900  
Db 158540 AGGTAGATTTCCCAACCAAAATATATCCAGAGATGCCCTTTGTCAATGGGTTATATACAGC 158599  
QY 901 CTTTGGCTCTCTGAGTCAATGTATTTACCACTTTTCCCTGAGAAATCGAAATCAATTTGG 960  
Db 158600 CTTTGGCTCTCTGAGTCAATGTATTTACCACTTTTCCCTGAGAAATCGAAATCAATTTGG 158659  
QY 961 GGAGCGGACATTTAGAAAAGAAATCAAGTGTCAATGATTAATCAAAATCTTCAATAGAT 1020  
Db 158660 GGAGCGGACATTTAGAAAAGAAATCAAGTGTCAATGATTAATCAAAATCTTCAATAGAT 158719  
QY 1021 GCAGTTATTCAGATGGCCAAAGGAAATAAAGTCATTAAGTGGGTGGTGAATTTAG 1080  
Db 158720 GCAGTTATTCAGATGGCCAAAGGAAATAAAGTCATTAAGTGGGTGGTGAATTTAG 158779  
QY 1081 AACATGCTGTTTTTCAGGTTATGCTCTTTTTTTTTTTTTTTTTTTTTTTTTTAAATAGGAAATG 1140  
Db 158780 AACATGCTGTTTTTCAGGTTATGCTCTTTTTTTTTTTTTTTTTTTTTTTTTTAAATAGGAAATG 158839  
QY 1141 TGTGTTGTCAGAGCCCAATGTCATTCAAAAGAGCTCTCTCTTTTTTCTGTGTCAGTCATGTG 1200  
Db 158840 TGTGTTGTCAGAGCCCAATGTCATTCAAAAGAGCTCTCTCTTTTTTCTGTGTCAGTCATGTG 158899  
QY 1201 CTGGGACAGAGAGGGATCTGGATAGGCAACATCATAGATTTGCTCTGAGCTGCTCTTT 1260  
Db 158900 CTGGGACAGAGAGGGATCTGGATTTAGGCAACATCATAGATTTGCTCTGAGCTGCTCTTT 158959  
QY 1261 GGTGATTAACCTTCCAAATCTTAACTTTTGGAAATTCACAACTCAAGCTCAAGAGGAAACCT 1320  
Db 158960 GGTGATTAACCTTCCAAATCTTAACTTTTGGAAATTCACAACTCAAGCTCAAGAGGAAACCT 159019

QY 1321 ACTCTCTGATCTACCACTATGTTCTGCAATTTTCTATCATGGTCTATGGAACCTTCTCTTA 1380  
Db 159020 ACTCTCTGATCTACCACTATGTTCTGCAATTTTCTATCATGGTCTATGGAACCTTCTCTTA 159079  
QY 1381 GAAATCCAGTGGCAAGAGTTCATGATTAAGAGTGTCTGAGCTCAGGCCAGGCAAGTCAAT 1440  
Db 159080 GAAATCCAGTGGCAAGAGTTCATGATTAAGAGTGTCTGAGCTCAGGCCAGGCAAGTCAAT 159139  
QY 1441 GAACTACTTCTGAGTTATTTACTACTGATTTGFGGGCAGCCTCAGCTATCGGTTCTTTC 1500  
Db 159140 GAACTACTTCTGAGTTATTTACTACTGATTTGFGGGCAGCCTCAGCTATCGGTTCTTTC 159199  
QY 1501 ACACCTGCTTATGAGAGTATCCATATTTATGTCGAGGCCAGTAAATGTCCTCCACGAGA 1560  
Db 159200 ACACCTGCTTATGAGAGTATCCATATTTATGTCGAGGCCAGTAAATGTCCTCCACGAGA 159259  
QY 1561 TCAGTTTCTCAACTAACCTCGAATTTTTTATGGGTTTTTATGCTTATGCTTAAATCA 1620  
Db 159260 TCAGTTTCTCAACTAACCTCGAATTTTTTATGGGTTTTTATGCTTAAATCA 159319  
QY 1621 ACATTAACAGTCTTCCCTCTGTATTTCTCCTGTAACAAATTAAGGCTGCAAAAAA 1680  
Db 159320 ACATTAACAGTCTTCCCTCTGTATTTCTCCTGTAACAAATTAAGGCTGCAAAAAA 159379  
QY 1681 ATCTTTTTAAAAATTAATGCCATAAAGTATTTGCTCTGGGCTACTGTATGCTTCTTTTC 1740  
Db 159380 ATCTTTTTAAAAATTAATGCCATAAAGTATTTGCTCTGGGCTACTGTATGCTTCTTTTC 159439  
QY 1741 TTTTCTCTCTTTTCACTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1800  
Db 159440 TTTTCTCTCTTTTCACTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 159499  
QY 1801 ACTATGCTGAGTCTCCTCAAGCAGGCTCACATAGTGAAGTGGAGTGGGCTACG 1860  
Db 159500 ACTATGCTGAGTCTCCTCAAGCAGGCTCACATAGTGAAGTGGAGTGGGCTACG 159559  
QY 1861 GAAGAAACAGAAACCTCTAGTTTATTTAAACCTGTATTTACTGCCCCTTCCCTTTA 1920  
Db 159560 GAAGAAACAGAAACCTCTAGTTTATTTAAACCTGTATTTACTGCCCCTTCCCTTTA 159619  
QY 1921 GACTTGACCATATGACCTCCTGCTCCCATTTAAGCATAGGGCAGGCTTTATTTTACA 1980  
Db 159620 GACTTGACCATATGACCTCCTGCTCCCATTTAAGCATAGGGCAGGCTTTATTTTACA 159679  
QY 1981 ATGGTAAATAGATATCACTGAGGTTTTATCAAGAGTTGCGGCGGTCGTGAAAGTTCAC 2040  
Db 159680 ATGGTAAATAGATATCACTGAGGTTTTATCAAGAGTTGCGGCGGTCGTGAAAGTTCAC 159739  
QY 2041 AACACAGATTCAGGTTTTGTTGCGCAGATCTCAATTTTACATGTTTCTTTGCGCAAGG 2100  
Db 159740 AACACAGATTCAGGTTTTGTTGCGCAGATCTCAATTTTACATGTTTCTTTGCGCAAGG 159799  
QY 2101 GTGATTTTTTAAATAACATTTGTTTCTCTTATCTTCTTTTATTTAGTTCGGAGACCAT 2160  
Db 159800 GTGATTTTTTAAATAACATTTGTTTCTCTTATCTTCTTTTATTTAGTTCGGAGACCAT 159859  
QY 2161 GAGAAACAGGCTCAATCATCTTTTATGATCCCAAGTGAAGGCAAGCCCTCCAGAGA 2220  
Db 159860 GAGAAACAGGCTCAATCATCTTTTATGATCCCAAGTGAAGGCAAGCCCTCCAGAGA 159919  
QY 2221 GCGTTATCTGACCCCAACCCAGCAGACATTTGTCAGACACCTTCGGGGCTGTCTGAAAGCC 2280  
Db 159920 GCGTTATCTGACCCCAACCCAGCAGACATTTGTCAGACACCTTCGGGGCTGTCTGAAAGCC 159979  
QY 2281 ATAGCCTCCAGGAGAGCCCT 2301  
Db 159980 ATAGCCTCCAGGAGAGCCCT 160000

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 124859

LENGTH: 1339

TYPE: DNA

ORGANISM: Human

US-10-027-632-124859

Query Match

Best Local Similarity 31.6%; Score 727.4; DB 13; Length 1339;

Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1

CTGAATGATGCTCCCAAGTGTATGTATGATGAGTCTTCTGTGTGCCAGTGGAAATAGTGTG 60

DB

611

CTGAATGATGCTCCCAAGTGTATGTATGATGAGTCTTCTGTGTGCCAGTGGAAATAGTGTG 670

QY

61

TGTCATGTGTCATTTTAAAGACTTAAATACACTAATATAGTCTTCTCTCTTTGG 120

DB

671

TGTCATGTGTCATTTTAAAGACTTAAATACACTAATATAGTCTTCTCTCTTTGG 730

QY

121

ATAATAGCAGCTTGTTCCTGATGAGTCTTGAAGCCCTAGGTCCAGAGAGCCCTTGAGA 180

DB

731

ATAATAGCAGCTTGTTCCTGATGAGTCTTGAAGCCCTAGGTCCAGAGAGCCCTTGAGA 790

QY

181

ATTTACTTCCCAAAAGGCAACAGACCGTGAATAATAGATGCCAATGTGTCAGCAAAAG 240

DB

791

ATTTACTTCCCAAAAGGCAACAGACCGTGAATAATAGATGCCAATGTGTCAGCAAAAG 850

QY

241

ACAGAGAGTGTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 300

DB

851

ACAGAGAGTGTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 910

QY

301

TGCTTTTCAATCAGTTTAAACAGCCCTCTGAACTCCTTCTTATCATGTATCGCTTCTG 360

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 124859

LENGTH: 1339

TYPE: DNA

ORGANISM: Human

US-10-027-632-124859

Query Match

Best Local Similarity 31.6%; Score 727.4; DB 13; Length 1339;

Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1

CTGAATGATGCTCCCAAGTGTATGTATGATGAGTCTTCTGTGTGCCAGTGGAAATAGTGTG 60

DB

611

CTGAATGATGCTCCCAAGTGTATGTATGATGAGTCTTCTGTGTGCCAGTGGAAATAGTGTG 670

QY

61

TGTCATGTGTCATTTTAAAGACTTAAATACACTAATATAGTCTTCTCTCTTTGG 120

DB

671

TGTCATGTGTCATTTTAAAGACTTAAATACACTAATATAGTCTTCTCTCTTTGG 730

QY

121

ATAATAGCAGCTTGTTCCTGATGAGTCTTGAAGCCCTAGGTCCAGAGAGCCCTTGAGA 180

DB

731

ATAATAGCAGCTTGTTCCTGATGAGTCTTGAAGCCCTAGGTCCAGAGAGCCCTTGAGA 790

QY

181

ATTTACTTCCCAAAAGGCAACAGACCGTGAATAATAGATGCCAATGTGTCAGCAAAAG 240

DB

791

ATTTACTTCCCAAAAGGCAACAGACCGTGAATAATAGATGCCAATGTGTCAGCAAAAG 850

QY

241

ACAGAGAGTGTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 300

DB

851

ACAGAGAGTGTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAACACCTT 910

QY

301

TGCTTTTCAATCAGTTTAAACAGCCCTCTGAACTCCTTCTTATCATGTATCGCTTCTG 360

DB

911

TGCTTTTCAATCAGTTTAAACAGCCCTCTGAACTCCTTCTTATCATGTATCGCTTCTG 970

QY

361

TTTATAGAGACTTAAACAGAGACATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 420

DB

971

TTTATAGAGACTTAAACAGAGACATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1030

QY

421

AATGTTTTTCTTGTGTATTTTAAACAGGGCTGAAGACATTTATGGAGAAAGACTTGAATA 480

DB

1031

AATGTTTTTCTTGTGTATTTTAAACAGGGCTGAAGACATTTATGGAGAAAGACTTGAATA 1090

QY

481

TCATAGAGAGAGAGAGACTGTTTCCAGCTTGGGAAAAGTGTATTTATCAGCAGTTAGT 540

DB

1091

TCATAGAGAGAGAGAGACTGTTTCCAGCTTGGGAAAAGTGTATTTATCAGCAGTTAGT 1150

QY

541

GACAGAGAGAGAGAGACTGTTTCCAGCTTGGGAAAAGTGTATTTATCAGCAGTTAGT 600

DB

1151

GACAGAGAGAGAGAGACTGTTTCCAGCTTGGGAAAAGTGTATTTATCAGCAGTTAGT 1210

Db 911 TGCCTTTCAATCAGTTTAAACAGCCTCCTGAACTCCTCTCTATCATGGTACGCTTCCTG 970  
QY 361 TTTTAGAGAGACTAACAGAGACATTGAAAGTCAGGTAAGCTGAATATTAACATTGCTGA 420  
Db 971 TTTTAGAGAGACTAACAGAGACATTGAAAGTCAGGTAAGCTGAATATTAACATTGCTGA 1030  
QY 421 AATGTTTTTCCCTGTGTTATTTTAAACAGGCTGAACACATTATGGAAGAAAGCTGAATAA 480  
Db 1031 AATGTTTTTCCCTGTGTTATTTTAAACAGGCTGAACACATTATGGAAGAAAGCTGAATAA 1090  
QY 481 TCATAAGAAAGAAAGACTGTTTCAAGCTTCGGAAGAAAGTGTATTTATCAGCAGTTAGT 540  
Db 1091 TCATAAGAAAGAAAGACTGTTTCAAGCTTCGGAAGAAAGTGTATTTATCAGCAGTTAGT 1150  
QY 541 GAGAGAGAAAGAAATCAGAAAGTTTCAGAGAAACACCTAAGACAAACAGGTAAAGAGG 600  
Db 1151 GAGAGAGAAAGAAATCAGAAAGTTTCAGAGAAACACCTAAGACAAACAGGTAAAGAGG 1210  
QY 601 AAGGAAGAAAGAAATTAGGTAAGAGTTTCAAGAAACACTAGCCCGAGTCAGTATGCCAG 660  
Db 1211 AAGGAAGAAAGAAATTAGGTAAGAGTTTCAAGAAACACTAGCCCGAGTCAGTATGCCAG 1270  
QY 661 CAGCCTGTTCTCCAGCCCTTCTTACCCTGGGAGGTGAAAGACTTAGAAACACAGTAGCAG 720  
Db 1271 CAGCCTGTTCTCCAGCCCTTCTTACCCTGGGAGGTGAAAGACTTAGAAACACAGTAGCAG 1330  
QY 721 AGGAGATCT 729  
Db 1331 AGGAGATCT 1339

## RESULT 4

US-10-136-819-3  
; Sequence 3, Application US/10136819  
; Publication No. US20030166593A1  
; GENERAL INFORMATION:  
; APPLICANT: Chien, Kenneth  
; APPLICANT: Hoshijima, Masahiko  
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gene  
; FILE REFERENCE: 6627-PAL198  
; CURRENT APPLICATION NUMBER: US/10/136,819  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: 60/287,423  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1250  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-136-819-3

Query Match 6.9%; Score 159; DB 15; Length 1250;  
Best Local Similarity 97.0%; Pred. No. 5.3e-31;  
Matches 162; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 128 GCAGTTGTTCCGTATGAGCTTGAAGCCCTAGTCCCAAGAGAGCCCTTGAGAAATTTACT 187  
Db 568 GCAGTTGTTCCGTATGAGCTTGAAGCCCTAGTCCCAAGAGAGCCCTTGAGAAATTTACT 627  
QY 188 TCCCAAAAGGCAACAGACCCGTGAATAGATGCAATGTGCTAGCCCAAAAGACAAAGAA 247  
Db 628 TCCCAAAAGGCAACAGACCCGTGAATAGATGCAATGTGCTAGCCCAAAAGACAAAGAA 687  
QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 294  
Db 688 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 734

## RESULT 5

US-09-749-728B-66  
; Sequence 66, Application US/09749728B  
; Patent No. US20020142457A1

## ; GENERAL INFORMATION:

; APPLICANT: Umezawa, Akihiro  
; APPLICANT: Hata, Jun-ichi  
; APPLICANT: Fukuda, Keiichi  
; APPLICANT: Ogawa, Satoshi  
; APPLICANT: Sakurada, Kazuhiro  
; APPLICANT: Gojo, Satoshi  
; APPLICANT: Yamada, Yoji

; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES  
; FILE REFERENCE: 00766.000043  
; CURRENT APPLICATION NUMBER: US/09/749,728B  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: H11-372826

; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: PCT-JP00-01148  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: PCT-JP00-07741  
; PRIOR FILING DATE: 2000-11-02  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver.2.0  
; SEQ ID NO 66

; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; OTHER INFORMATION: (1)..(639)

US-09-749-728B-66

Query Match 6.8%; Score 157.4; DB 9; Length 636;

Best Local Similarity 96.4%; Pred. No. 8.8e-31;  
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 GCAGTTGTTCCGTATGAGCTTGAAGCCCTAGTCCCAAGAGAGCCCTTGAGAAATTTACT 187

Db 234 GCAGTTGTTCCGTATGAGCTTGAAGCCCTAGTCCCAAGAGAGCCCTTGAGAAATTTACT 293

QY 188 TCCCAAAAGGCAACAGACCCGTGAATAGATGCCAATGTGCTAGCCCAAAAGACAAAGAA 247

Db 294 TCCCAAAAGGCAACAGACCCGTGAATAGATGCCAATGTGCTAGCCCAAAAGACAAAGAA 353

QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 294

Db 354 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 400

## RESULT 6

US-10-295-942-1  
; Sequence 1, Application US/10295942  
; Publication No. US20030109480A1  
; GENERAL INFORMATION:

; APPLICANT: Corder, Roger  
; APPLICANT: Smith, Adrian  
; APPLICANT: Higenbottom, Tim  
; APPLICANT: Rothblatt, Martine  
; APPLICANT: Vane, John  
; APPLICANT: Jones, Delphine

; TITLE OF INVENTION: INHIBITORS OF ENDOTHELIN-1 SYNTHESIS  
; FILE REFERENCE: 080618/0123  
; CURRENT APPLICATION NUMBER: US/10/295,942

; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US/09/527,240

; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1

; LENGTH: 1166  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-295-942-1

Query Match 6.8%; Score 157.4; DB 15; Length 1166;

Best Local Similarity 96.4%; Pred. No. 1.3e-30;

Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 128 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 187  
Db 485 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 544  
Qy 188 TCCACAAAGGCAACAGCCGTTGAAATAGATGCCAATGTGCTAGCCCAAAAGACAAGAA 247  
Db 545 TCCACAAAGGCAACAGCCGTTGAAATAGATGCCAATGTGCTAGCCCAAAAGACAAGAA 604  
Qy 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 294  
Db 605 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 651

RESULT 7  
US-10-211-462-126  
; Sequence 126, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 126  
; LENGTH: 1251  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-211-462-126

Query Match 6.8%; Score 157.4; DB 13; Length 1251;  
Best Local Similarity 96.4%; Pred. No. 1.4e-30;  
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 128 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 187  
Db 570 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 629  
Qy 188 TCCACAAAGGCAACAGCCGTTGAAATAGATGCCAATGTGCTAGCCCAAAAGACAAGAA 247  
Db 630 TCCACAAAGGCAACAGCCGTTGAAATAGATGCCAATGTGCTAGCCCAAAAGACAAGAA 689  
Qy 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 294  
Db 690 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 736

RESULT 8  
US-10-342-887-701  
; Sequence 701, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.

; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 701  
; LENGTH: 1251  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-701

Query Match 6.8%; Score 157.4; DB 13; Length 1251;  
Best Local Similarity 96.4%; Pred. No. 1.4e-30;  
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 128 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 187  
Db 570 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 629  
Qy 188 TCCACAAAGGCAACAGCCGTTGAAATAGATGCCAATGTGCTAGCCCAAAAGACAAGAA 247  
Db 630 TCCACAAAGGCAACAGCCGTTGAAATAGATGCCAATGTGCTAGCCCAAAAGACAAGAA 689  
Qy 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 294  
Db 690 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA 736

RESULT 9  
US-10-172-118-701  
; Sequence 701, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van 't Veer, Laura  
; APPLICANT: Van de Vijver, Marc  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-178-999  
; CURRENT APPLICATION NUMBER: US/10/172,118  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/380,770  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 701  
; LENGTH: 1251  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM\_001955  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-701

Query Match 6.8%; Score 157.4; DB 13; Length 1251;  
Best Local Similarity 96.4%; Pred. No. 1.4e-30;  
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 128 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 187  
Db 570 GCACGTTGTTCCGTTATGGACTTGGAGCCCTTAGTCCAAAGAGCCCTTGGAGATTACT 629

Qy	188	TCCCAAAAGGCAACAGACCGTGGAAATAGATGCAATGTGCTAGCCAAAGACCAAGAA	247
Db	630	TCCCAAAAGGCAACAGACCGTGGAAATAGATGCAATGTGCTAGCCAAAGACCAAGAA	689
Qy	248	GTGCTGGAAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA	294
Db	690	GTGCTGGAAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAA	736

```

RESULT 10
US-10-170-385-398
; Sequence 398, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170/385
; CURRENT FILING DATE: 2002-06-12
; PRIORITY APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 398
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-398

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	Query Match	6.8%	Score 157.4	DB 13	Length 1251
	Best Local Similarity	96.4%	Pred. No. 1.4e-30		
	Matches 161	Conservative 0	Mismatches 6	Indels 0	Gaps 0
QY	128	GCACGTTGTTCCGTTATGCACTTGGAAAGCCCTAGGTCACAGAGAGCGCTTGGAGAAATTACT	187		
Db	570	GCACGTTGTTCCGTTATGCACTTGGAAAGCCCTAGGTCACAGAGAGCGCTTGGAGAAATTACT	629		
QY	188	TCCACAAAGGCAACAGACCGTGAAAAATAGATCCCAATGTCTAGCCAAAAGACACAGAA	247		
Db	630	TCCACAAAGGCAACAGACCGTGAGATAGATGCCAATGTCTAGCCAAAAGACACAGAA	689		
QY	248	GTGCTGGAATTTTTTCCAAAGCAGGAAAGAACTCAGGTCAGCAGAA	294		
Db	690	GTGCTGGAATTTTTTCCAAAGCAGGAAAGAACTCAGGCTGAAGACA	736		

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RESULT 11
US-10-007-926A-458
; Sequence 458, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGAITE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007.926A

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, CURRENT FILING DATE: 2001-12-07
, PRIOR APPLICATION NUMBER: 60/254,090
, PRIOR FILING DATE: 2000-12-08
, NUMBER OF SEQ ID NOS: 468
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 458
, LENGTH: 1251
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: 3' terminal sequence
, FEATURE:
, OTHER INFORMATION: endothelin 1 (EDN1)
US-10-007-926A-458

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Query Match	6.8%;	Score 157.4;	DB 15;	Length 1251;
Best Local Similarity	96.4%;	Pred. No. 1.4e-30;		
Matches 161;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

  

QY	128	GCACGTTCTCCGTATGGACTTGGAGGCCCTAGGTC	CNAGAGAGCGCTTGGAGAATTACT	187
Dd	570	GCACGTTCTCCGTATGGACTTGGAGGCCCTAGGTC	CAAGAGAGCGCTTGGAGAATTACT	629
QY	188	TCCCACAAGSCAACACACCGTGAAATAATAGATG	CCCAATGCTAGGCCAAAAAGACAA	247
Dd	630	TCCCACAAGSCAACACACCGTGAGTAATAGATG	CCCAATGCTAGGCCAAAAGACAA	689
QY	248	GTGCTGAATTTTTGCCAAGCAGGAAAAGAACTC	AGGTGAGCAGAAA	294
Dd	690	GTGCTGAATTTTTGCCAAGCAGGAAAAGAACTC	AGGTGAGCAGAAA	736

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RESULT 12
US-101-101-510-5
; Sequence 5, Application US/10101510
; Publication NO. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/216,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Homo sapiens
US-101-101-510-5

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Query Match	6.8%;	Score 157.4;	DB 15;	Length 1251;
Best Local Similarity	96.4%;	Prod. No. 1.4e-30;		
Matches 161;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	128	GCACGTTGTTCCGTTATGGAACTTGGAAAGCCCTTAGGTCCAAAGAGAGCGCTTGGAGAAATTTACT	187	
Db	570	GCACGTTGTTCCGTTATGGAACTTGGAAAGCCCTTAGGTCCAAAGAGAGCGCTTGGAGAAATTTACT	629	
QY	188	TCCACAAAAGGCACACAGCCGTGCAAAATAGATGCCAAATGCTGTAGCCAAAAGACACAGAA	247	
Db	630	TCCACAAAAGGCACACAGCCGTGAGAAATAGATGCCAAATGCTGTAGCCAAAAGACACAGAA	689	
QY	248	GTGCTGGAATTTTTGCCAAGCAGGAAAAGAACTCAGGTGAGCAGAAA	294	
Db	690	GTGCTGGAATTTTTGCCAAGCAGGAAAAGAACTCAGGGCTGAAGACA	736	
RESULT 13				
US-10-021-660-40				
: Sequence 40, Application US/10021660				

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; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
; Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 019501-000710US
; CURRENT APPLICATION NUMBER: US/10/021.660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784.356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-021-660-40

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Best Local Similarity 96.4%; Pred. No. 1.4e-30;
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 GCACGTTGTTCCGTTAGTGGACCTTGAAGCCCTAGTCCAAAGAGAGCCCTTGGAGAAATTTACT 187
DB 570 GCACGTTGTTCCGTTAGTGGACCTTGAAGCCCTAGTCCAAAGAGAGCCCTTGGAGAAATTTACT 629

QY 188 TCCCAAAAGGCAACAGACCGGTGAAATAGATGCCAATGTCTAGCCAAAAGACAAGAA 247
DB 630 TCCCAAAAGGCAACAGACCGGTGAAATAGATGCCAATGTCTAGCCAAAAGACAAGAA 689

QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 294
DB 690 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 736

RESULT 14
US-10-060-036-22
; Publication US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 508, 553
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-22

Query Match          6.8%; Score 156.4; DB 15; Length 566;
Best Local Similarity 96.4%; Pred. No. 1.5e-30;
Matches 160; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 129 CACGTTGTTCCGTTAGTGGACCTTGAAGCCCTAGTCCAAAGAGAGCCCTTGGAGAAATTTACT 188
DB 1 CACGTTGTTCCGTTAGTGGACCTTGAAGCCCTAGTCCAAAGAGAGCCCTTGGAGAAATTTACT 60

QY 189 CCAACAAAGGCAACAGACCGGTGAAATAGATGCCAATGTCTAGCCAAAAGACAAGAA 248
DB 61 CCAACAAAGGCAACAGACCGGTGAAATAGATGCCAATGTCTAGCCAAAAGACAAGAA 120

QY 249 TGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 294
DB 121 TGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 166

RESULT 15
US-09-918-995-21013
; Sequence 21013, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21013
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(512)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-21013

Query Match          6.8%; Score 155.8; DB 10; Length 512;
Best Local Similarity 95.8%; Pred. No. 2e-30;
Matches 160; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 128 GCACGTTGTTCCGTTAGTGGACCTTGAAGCCCTAGTCCAAAGAGAGCCCTTGGAGAAATTTACT 187
DB 157 GCACGTTGTTCCGTTAGTGGACCTTGAAGCCCTAGTCCAAAGAGAGCCCTTGGAGAAATTTACT 216

QY 188 TCCCAAAAGGCAACAGACCGGTGAAATAGATGCCAATGTCTAGCCAAAAGACAAGAA 247
DB 217 TCCCAAAAGGCAACAGACCGGTGAAATAGATGCCAATGTCTAGCCAAAAGACAAGAA 276

QY 248 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 294
DB 277 GTGCTGGAATTTTCCCAAGCAGGAAAGAACTCAGGTGAGCAGAAA 323

Search completed: July 16, 2004, 23:09:17
Job time : 1006 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2004, 15:06:54 ; Search time 5805 Seconds  
(without alignments)  
11836.844 Million cell updates/sec

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Perfect score: 2301  
Sequence: 1 ctgaaatgatgctcccaagt.....tagctccacggagagccct 2301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_pig:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

5 395 17.2 549 14 R56187

6 316.6 13.8 425 14 R55914

7 284.4 12.4 438 14 CB852037

8 281.6 12.2 518 28 A0615825

9 279.8 12.2 291 14 F06636

10 245 10.6 713 12 BM974937

11 184 8.0 412 14 R48157

12 180 7.8 202 12 B1040245

13 157.4 6.8 740 12 B1821379

14 157.4 6.8 740 12 BM718889

15 157.4 6.8 769 14 CB988507

16 157.4 6.8 826 10 BE904559

17 157.4 6.8 848 12 B1758161

18 157.4 6.8 891 12 B1818778

19 157.4 6.8 1053 9 AL543736

20 157.4 6.8 1087 12 BM546209

21 157.4 6.8 1138 9 AL548042

22 157.4 6.8 1154 12 BM545093

23 157.4 6.8 1190 9 AL550935

24 157.4 6.8 1201 13 BX439515

25 155.8 6.8 1109 12 BM805113

26 155 6.7 659 14 CD370121

27 155 6.7 665 14 CA426258

28 155 6.7 715 14 CA309734

29 155 6.7 758 12 BM680754

30 155 6.7 758 12 BQ009676

31 155 6.7 835 12 B868856

32 155 6.7 839 12 BGL18495

33 155 6.7 938 13 BX348929

34 155 6.7 959 13 BX348930

35 154 6.7 598 12 BM671893

36 154 6.7 603 9 AW043551

37 154 6.7 731 12 BM977229

38 154 6.7 837 9 AI039852

39 153.4 6.7 582 10 AW119009

40 153.4 6.7 646 13 BX098479

41 153.4 6.7 689 13 BU626469

42 153.4 6.7 756 14 CA431861

43 152.2 6.6 1201 9 AL533672

44 150.8 6.6 596 10 AW956848

45 150.8 6.6 808 9 AI521846

RESULT 1

AG061490

LOCUS Pan troglodytes DNA, clone: PTB-049121.R, genomic survey sequence. 661 bp DNA linear GSS 03-NOV-2001

DEFINITION

AG061490

ACCESSION

AG061490.1 GI:16613292

VERSION

GSS.

KEYWORDS

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB Unpublished

2 (bases 1 to 661)

TITLE

JOURNAL

REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

TITLE

JOURNAL

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suhei-ro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@gsic.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/. Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	568.8	24.7	661	29 AG061490	Pan trogl
C 2	544.8	23.7	624	29 AG157710	Pan trogl
C 3	530.4	23.1	532	28 B48925	Pan trogl
4	469.2	20.4	474	9 AW016885	AW016885 UI-B10p

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.









FEATURES  
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Location/Qualifiers  
1. .438  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-FNO-aes-p-20-0-UT"  
/tissue\_type="Human Lung Epithelial cells"  
/lab\_host="DH10B (Life Technologies) (TI phase resistant)"  
/clone\_lib="UI-CF-FNO"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and D11). The library was subtracted according to according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@iowa.edu  
TAG\_SEQ=None found"

## ORIGIN

Query Match 12.4%; Score 284.4; DB 14; Length 438;  
Best Local Similarity 98.0%; Pred. No. 2.2e-37;  
Matches 288; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 CTGAATGATGCTCCCAAGTGTATGATGAGCTCTTGTGTCGCCAGTGGATAGGTG 60  
DB 84 CTGAATGATGCTCCCAAGTGTATGATGAGCTCTTGTGTCGCCAGTGGATAGGTG 143  
QY 61 TGTCCATGTGTCATTTTAAAGACTATTAAATACACTAATATAGTTCCTTCTCTTTGG 120  
DB 144 TGTCCATGTGTCATTTTAAAGACTATTAAATACACTAATATAGTTCCTTCTCTTTGG 203  
QY 121 ATAATAGGACGTTGTTCCGATGAGCTTGAAGCCCTAGTGTCCCAAGAGCCCTGGAGA 180  
DB 204 ATAATAGGACGTTGTTCCGATGAGCTTGAAGCCCTAGTGTCCCAAGAGCCCTGGAGA 263  
QY 181 ATTACTTCCCAAGGCAACAGACCGTGAAATAGATGCCAATGTGTCAGCAAAAAG 240  
DB 264 ATTACTTCCCAAGGCAACAGACCGTGAAATAGATGCCAATGTGTCAGCAAAAAG 323  
QY 241 ACAAGAGTGTGGAATTTTGGCAAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 294  
DB 324 ACAAGAGTGTGGAATTTTGGCAAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 377

RESULT 8  
AQ615825/c

LOCUS  
DEFINITION HS:5146\_B2\_C10\_SP6E RPCI-11 Human Male BAC Library Homo sapiens  
Genomic\_clone Plate=722 Col=20 Row=F, genomic survey sequence.  
ACCESSION AQ615825  
VERSION AQ615825.1 GI:5077101  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
9330589  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu

## TITLE

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
9330589  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Research Genetics (<http://www.htsc.washington.edu>). BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 722 row: F column: 20  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 518.

FEATURES  
source

Location/Qualifiers  
1. .518  
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/sex="male"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

## ORIGIN

Query Match 12.2%; Score 281.6; DB 28; Length 518;  
Best Local Similarity 87.2%; Pred. No. 5.9e-37;  
Matches 333; Conservative 0; Mismatches 44; Indels 5; Gaps 2;  
QY 929 CACTTTCCCTGAGAAATCGAAATCATTTGGGGAGCGGACATTTAGAAAAGATCAAA 988  
DB 475 CCCCTTTCCTGAGAAATCAAAATCATTTGGGGGCGGACATTTAGAAAAGATCAAA 416  
QY 989 GT-GTCATGGATPAATCAAAATTTTCAATAGTTGCAGTTATTTCAGATGCCCCAAGGAAAA 1047  
DB 415 GTGGTCTGGAGATCCAAATTTCTCAATAGTTGCAGTTATTTCAGATGCCCCAAGGAAAA 356  
QY 1048 ATAAAGTCTAGTAGAGGTTGGTAGAATTTAGAACATGCTGTTTTCAGGTTATGGTC 1107  
DB 355 ATAAAGTCTTAGTAGAGGTTGGTAGAATTTAGAACATGCTGTTTTCAGGTTATGGTC 296  
QY 1108 T-----TTTTTTTTTTTTTTTTTAAATAGGAAATGTGTTTGGTCAGAGCCCAATGTCA 1163  
DB 295 TTCTCTATTTTACTTTTATATATATACATAGGAAATGTGTTTGGTCAGAGCCCAATGTCA 236  
QY 1164 TTCCAAAAGCTCTCTTTTCTGGTCAGTCATGCTGGGACAGAGAGGATCTGGA 1223  
DB 235 TTCCGAAAAGCTCTCTTTTCTGGTCAGTCATGCTGGGACAGAGAGGATCTGGA 176  
QY 1224 TTAGGCAACATCATAGAGTTGCTCTGAGCTGCTCTTTGGTGATACCCCTTCCAATCTTA 1283  
DB 175 TTAGGCAACATCATAGAGTTGCTCTGAGCTGCTCTTTGGTGATACCCCTTCCAATCTTA 116  
QY 1284 AACTTTGGAAATCAACAGCT 1305  
DB 115 CCTATTAGGAATAACAGAGTCT 94

RESULT 9  
F06636

LOCUS  
DEFINITION HSC1F5031 normalized infant brain cDNA Homo sapiens cDNA clone  
c-1fe03, mRNA sequence.  
ACCESSION F06636  
VERSION F06636.1 GI:672236  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 291)  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,

Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pietu, G., Pouliot, Y.,  
Sebastiani-Kabakthchis, C. and Tessier, A.  
IMAGE: Molecular integration of the analysis of the human genome  
and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
95277534  
MEDLINE  
PUBMED  
COMMENT  
Contact: Genethon  
Genexpross-Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpross@genethon.fr  
Single read  
Genexpross\_library\_id: C; Genexpross\_sequence\_id: ylc-1fe03  
Seq primer: (-21)M13-universal.  
Location/Qualifiers  
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Site 2: NotI; sex=Female; dev stage=3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization method:  
Bento Soares, P.N.A.S in press"

FEATURES

source

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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/sex="Female"  
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/clone\_lib="normalized infant brain cDNA"  
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Site 2: NotI; sex=Female; dev stage=3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization method:  
Bento Soares, P.N.A.S in press"

ORIGIN

Query Match 12.2%; Score 279.8; DB 14; Length 291;  
Best Local Similarity 96.6%; Pred. No. 1.6e-36;  
Matches 281; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
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Db 1 TTINTGAATACCTGGATTTTATGGTTTATTATGCGCACTATTAAATCAACAT 60  
QY 1625 TACAGTTCTCCCTCTGATTTCTCTGTAACCAATTAGGCTGCAAAAAAATCT 1684  
Db 61 TACAGTTCTCCCTCTGATTTCTCTGTAACCAATTAGGCTGCAAAAAAATCT 120  
QY 1685 TTTTAAATAATTCCTAAGTATTTCTCTGCGCTACTGATGCTTTCTTTT 1744  
Db 121 TTTTAAATAATTCCTAAGTATTTCTCTGCGCTACTGATGCTTTCTTTT 180  
QY 1745 TCTCTCTTTTCAACTAAGTCACCGCTCAATTTATTAGATGGCCATTAACAT 1804  
Db 181 NCTCTCTTTTCAACTAAGTCACCGCTCAATTTATTAGATGGCCATTAACAT 240  
QY 1805 ATGCTGAGTTCTCAAGGAGGCTACATAGTATGATGAAGTTGGATGGG 1855  
Db 241 ATGCNAAGTTCTCAAGGAGGCTCGCATAGTATGATGAAGTTGGATGGG 291

RESULT 10

BM974937/c  
LOCUS  
DEFINITION  
UI-CF-EC1-acd-d-12-0-UI.s1 UI-CF-EC1 Homo sapiens cdna clone  
BM974937  
UI-CF-EC1-acd-d-12-0-UI 3', mRNA sequence.  
ACCESSION  
BM974937.1 GI:19592528  
VERSION  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 713)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
MEDLINE  
PUBMED  
COMMENT  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.  
Location/Qualifiers  
1..713  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EC1-acd-d-12-0-UI"  
/tissue\_type="Adult and Fetal"  
/dev\_stage="Adult and Fetal"  
/lab\_hosts="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EC1"  
/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-EC1 is a normalized cDNA library containing the  
following tissue(s): Normal lung from adult and from fetal  
day 64, day 87, week 19 and week 42. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
AAGTGGCTTAC.  
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371  
and 380-383  
TAG LIB=UI-CF-EC1  
TAG\_SEQ=AAGTGGCTTAC"

ORIGIN

Query Match 10.6%; Score 245; DB 12; Length 713;  
Best Local Similarity 98.2%; Pred. No. 5.5e-31;  
Matches 267; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
QY 2031 GAAAGTTCAACACAGATTCAGGTTTGTGTGCGCAGATTCATAATTTACATGTTCTT 2090  
Db 713 GAAAGTTCAACACAGATTCAGG-TTGTGTGCGCAGATTCATAATTTACATGTTCTT 655  
QY 2091 TTGCGAA-AGGGTGATTTTTTAAATAACATTTTCTTCTTATCTTCTTTATTAGG 2149  
Db 654 NTGCCAANAGGGTGATTTTTTAAATAACATTTTCTTCTTATCTTCTTTATTAGG 595  
QY 2150 TCGGAGACCATGAGAAACAGCGTCAATCATCTTTTCATCATCCAGCTGAAGGCAAG 2209  
Db 594 TCGGAGACCATGAGAAACAGCGTCAATCATCTTTTCATCATCCAGCTGAAGGCAAG 535  
QY 2210 CCCTCCAGAGAGCGTTATGTGACCCACACCGAGCATTGGTGACAGACCTTCGGGGCC 2269

Db 534 CCTCCAGAGCGTGTATGTGACCCACAGCAGACATTTGGTACAGACCTTCGGGGCC 475

QY 2270 TGTCTGAAGCCATAGCCTCCACGGAGAGCCCT 2301

Db 474 TGTCTGAAGCCATAGCCTCCACGGAGAGCCCT 443

RESULT 11

R48197/c

LOCUS

DEFINITION

YJ63C09.r1 Soares breast 2NbHst Homo sapiens cDNA clone

IMAGE:153424 5' similar to gb:S56805 ENDOTHELIN-1 PRECURSOR

(HUMAN); mRNA sequence.

R48197

R48197.1 GI:810223

VERSION

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 412)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 849

High quality sequence stops: 274

Source

Location/Qualifiers

1..412

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:565741"

/db\_xref="taxon:9606"

/clone="IMAGE:153424"

/sex="Female"

/dev\_stage="adult"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares Breast 2NbHst"

/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 8.0%; Score 184; DB 14; Length 412;

Best Local Similarity 100.0%; Pred. No. 9.4e-21;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAATGATCTCCCAAGTCTATGTGATGAGCTCTCTGTGCGCCAGTGAATAGGTG 60

Db 184 CTGAATGATGCTCCCAAGTCTATGTGATGAGCTCTCTGTGCGCCAGTGAATAGGTG 125

QY 61 TGTCCATGTGTCATTTTAAAGACTATTAAATACACTAATATAGTTTCTCTCTTTGG 120

Db 124 TGTCCTATGTCTCATTTTAAAGACTATTAAATACACTAATATAGTTTCTCTCTTTGG 65

QY 121 ATAATAGGACAGCTTGTTCGTTATGGACTTGGAGCCCTAGGTCCAGAGAGCCCTTGGAGA 180

Db 64 ATAATAGGACAGCTTGTTCGTTATGGACTTGGAGCCCTAGGTCCAGAGAGCCCTTGGAGA 5

QY 181 ATTT 184

Db 4 ATTT 1

RESULT 12

BIO40245

LOCUS

DEFINITION

CM4-NT0287-010201-839-f02 NT0287 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BIO40245

VERSION

BIO40245.1 GI:14446871

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 202)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Sucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM4&t2=CM4-NT0287-010201-839-f02&t3=2001-02-01&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 202.

Location/Qualifiers

1..202

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="NT0287"

/note="Organ: nervous\_tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORISTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 7.8%; Score 180; DB 12; Length 202;

Best Local Similarity 94.9%; Pred. No. 6.5e-20;

Matches 186; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1822 GCAGGGTCACATAGTATGATGAAGTTGGATGGGCTACGGAGAACCCAGAACACTCTA 1881

Db 7 GCCGGGCCCATAGTATGATGAAGTTGGATGGGCTACGGATAGAAACCCAGAACACTCTA 66

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QY 1882 GTTATTATTAACCTGTATTACTGCCCACCTCCCTTAGACTGACCATATGACCCCTC 1941
Db 67 GTTATTATTAACCTGTATTACTGCCCACCTCCCTTAGACTGACCATATGACCCCTC 126

QY 1942 GTCCTCATTCAAGCATAGGGGAGGCTTTATTTTACAATGGTAATAGATATCACTTGA 2001
Db 127 GTCCTCATTCAAGCATAGGGGAGGCTTTATTTTACAATGGTAATAGATATCACTTGA 186

QY 2002 GGTTTTATCAAGAGT 2017
Db 187 GGTTTTATCAAGAGT 202

RESULT 13
BI821379 673 bp mRNA linear EST 04-OCT-2001
LOCUS 603038242F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178970 5',
DEFINITION mRNA sequence.
ACCESSION BI821379
VERSION BI821379.1 GI:15932929
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
REFERENCE 1 (bases 1 to 673)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11446 row: d column: 11
High quality sequence stop: 668.
FEATURES
location/Qualifiers
1..673
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5178970"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 6.8%; Score 157.4; DB 12; Length 673;
Best Local Similarity 96.4%; Pred. No. 1.8e-16; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 6;

QY 128 GCACGTTGTCGGTATGGAGCCCTAGGTCACAGAGAGCCTTGGAGAAATTTACT 187
Db 472 GCACGTTGTCGGTATGGAGCCCTAGGTCACAGAGAGCCTTGGAGAAATTTACT 531

QY 188 TCCCAAAAGGCAACAGACCGTGAAATAGATGCCAATGTGCTACCCAAAAGACAGAA 247
Db 532 TCCCAAAAGGCAACAGACCGTGAGAAATAGATGCCAATGTGCTACCCAAAAGACAGAA 591

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QY 248 GTCTCGAATTTTTCACAGAGAAAGAACTCAGGTGAGCAGAA 294
Db 592 GTCTCGAATTTTTCACAGAGAAAGAACTCAGGTGAGCAGCA 638

RESULT 14
BM718889 740 bp mRNA linear EST 01-MAR-2002
LOCUS UI-E-EO1-ajc-b-12-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
DEFINITION UI-E-EO1-ajc-b-12-0-UI 5', mRNA sequence.
ACCESSION BM718889
VERSION BM718889.1 GI:19037294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS Bernaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genom Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES
location/Qualifiers
1..740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EO1-ajc-b-12-0-UI"
/dev_stage="fetal"
/tissue_type="fetal eye"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EO1"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bernaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."

ORIGIN
Query Match 6.8%; Score 157.4; DB 12; Length 740;
Best Local Similarity 96.4%; Pred. No. 1.7e-16; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 6;

QY 128 GCACGTTGTCGGTATGGAGCCCTAGGTCACAGAGAGCCTTGGAGAAATTTACT 187
Db 486 GCACGTTGTCGGTATGGAGCCCTAGGTCACAGAGAGCCTTGGAGAAATTTACT 545

```

QY 188 TCCCAAGGCAACAGACCGGTGAATAGATGCAATGTCTAGCCCAAAAGACAGAA 247  
Db 546 TCCCAAGGCAACAGACCGGTGAATAGATGCAATGTCTAGCCCAAAAGACAGAA 605  
QY 248 GTGCTGGAATTTTCCCAAGCAGGAGAAAGAACTCAGGTGAGCAGAAA 294  
Db 606 GTGCTGGAATTTTCCCAAGCAGGAGAAAGAACTCAGGTGAGCAGAAA 652

RESULT 15  
CB988507  
LOCUS  
DEFINITION CB988507 769 bp mRNA linear EST 01-MAY-2003  
IMAGE:30340493 5', mRNA sequence.  
ACCESSION CB988507  
VERSION CB988507.1 GI:30283027  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 769)  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Stefan Hansson  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDA370 row: h column: 06  
High quality sequence stop: 620.  
Location/Qualifiers  
1..769  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30340493"  
/tissue\_type="Human Placenta"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_147"  
/note="Organ: placenta; Vector: pBluescriptR; Site 1:  
ali-XhoI; Site 2: BamH; Oligo-dT primed using primer  
5'-TTTTTTTTTTTNN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

## FEATURES

## source

## ORIGIN

Query Match 6.8%; Score 157.4; DB 14; Length 769;  
Best Local Similarity 96.4%; Pred. No. 1.6e-16;  
Matches 161; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 128 GCACGTTGTCGATGGACCTGGAAGCCCTAGGTCCAAAGAGAGCCCTTGGAGATTTACT 187  
Db 529 GCACGTTGTCGATGGACCTGGAAGCCCTAGGTCCAAAGAGAGCCCTTGGAGATTTACT 588  
QY 188 TCCCAAGGCAACAGACCGGTGAATAGATGCAATGTCTAGCCCAAAAGACAGAA 247  
Db 589 TCCCAAGGCAACAGACCGGTGAATAGATGCAATGTCTAGCCCAAAAGACAGAA 648  
QY 248 GTGCTGGAATTTTCCCAAGCAGGAGAAAGAACTCAGGTGAGCAGAAA 294  
Db 649 GTGCTGGAATTTTCCCAAGCAGGAGAAAGAACTCAGGTGAGCAGAAA 695